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DEFINITION Human TAIA-binding protein associated factor 11 30 complete cds.
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2263, 12352)
/gene="IAFII30"
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Best Local Similarity 100.0%; Pred. No. 4.02e-45:
Matches 98; Conservative 0; Mismatches 0
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/db_xref="taxon:9606"
/chromosome="li"
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1060. .1084
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2263. .2352)
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Link, Traces, 17939, 17934, 192426

Link, Traces, 17939, 17939, 17924, 179426
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                 24 - JUL - 1996
                                                                                                     Eshari in in the Hall wekamings Metadoa Cherdata
Vertekada, Eutheria, Frimatosi Catarrhini, Hominidae Homo
Adams.M.D.
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Iriton X-100:
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KEISDIANDALGHGKMKGTASJSSFSKSKTFFYTLTTMTLLTFALEETGIHVYFPHYFT
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Submitted (27-APR-1995) Laszlo Tora, CNRS Inserm ULP, Inst. de
Genetique et de Biologie Moleculaire et Cellulaire, Illkirch (ETEN)
                       (TAFTIRO) gene.
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Vertebrata: Mammalia: Eutherla, Frimutus: Gatarroloi: Homindae:
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16-JUN-1997
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                                                                                                                                     Exkarystae: Metazna, Chordata, Vertebrata: Mammalia: Eutheria: Redentia: Schroquath): Muridae: Murinae: Mus. (buss. 1 to 1750) (5.F. tibud., Mayne-R. and Wurd. (betification and characterization of a mouse protein kinase that is highly homologous to himan integrin-linked kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Urect Submission
Studicted (18-MAR-1907) Call Photogry University of Alabama at
Etrainabom, 1670 University Plvd., 217 Volker Hall. Birmingham, AL
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Veriobiata: Mammalia: Eutheria: Primates: Catarrhin; Hominidae;
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Hitters.P., Nortis.F., Buckley,W., Bocker, J., Cohnstone F.P., Pixer,E.F., Nortis.F., Buckley,W., Bocker, J., Johnson,M., Dobbins,J.R., Wyrick,T., Miller,J.R., Warker, J., Johnson,M., Dobbins,J., McClure,D., Liu,X., Strphensou,D. and Cleman,J., Potvalan,J., McClure,D., Liu,X., Strphensou,D. and Cleman,J., Forvalan, Lissue J., Holi, "Nom. (1997) In press 2. (bases 1.0.1451)
Holi, "Bon, To Ids.)
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Pred. No. 1.33e-30;
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/db_xref-"PTD:g218115"
//db_xref-"PTD:g218115"
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LLCGGVLLHDWVLTAAAHCKRNULQVFGKRHWYGKESSGDGSSVVRAVIHPRYDAAS
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HLVSREDCEHAYPGGITGNMLCAGDEKYGKDSCGGBSGGFLVFGBHLKGLVSWFNTIPFGSKEKPGVYTNVCRYTNWIGKTTGAK"
Direct Submission Submission, Ell Lilly and Company, Lilly Corporate Center, Indianapolis, IN 46285, USA
                                                                                                                                                                                                                        /tissue_type="Alzheimer's disrase brain tissue"
147. .81
//note="Zyme: protease bears hemotogy to Kallikhein class and an be levalized to microressels and microadila; chymotrypsin-like"
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhin; Hominidue; Homo.
1 (bases 1 to 756)
Jacq,X., Brou,C., Lutz,Y., Davidson,I., Chambon,P. and Tota,I.,
Human TAFII30 is present in a distinct TPIID complex and is
Cell 79 (1), 107-117 (1994)
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1'INSERM, Faculte de Medicine, 11 rue Humann, Strussbourg, 67-85
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DEFINITION Human TATA-binding protein associated factor 3P kba submit (tafi130) mRNA, complete cds.
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Bost Loral Similarity 100 0%: Pred. No. 2.21c-03;
Matches 31: Conservative 0: Mismatches 0: Indels o
                                                                                                                                                                                                                                                                                                                                                             /product="serine protease"
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                                                                                                             /organism="Homo sapiens"
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/db_xref="taxon:9606"
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18. .674
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productor persentation proliferator-actionable receptor gamma
/dl_xref="F1D.4562077"
/translation="MGCSGSGDPEAAPASAASAPGBAPVSAPAADESSTAAENKAS
AMGIAGGGAGAAAGGTFAARAGEPAFFRGAAPVSAAGGAAPBGALSNGVYULBSA
AMGDVKRVSSTPLVPFLMOLEDYTTTIPDANVTVYLNRAGEPREPPFIFILSLAAPA
RESELLAMFALGEFRENGERSKENDFKYTLTMFPLTPALSEYGINVKKPHYFT
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Stanton (Stray 1997) Department of Physiology, University of
Maryland, School of Medicine, 10 South Fine Street, MSTF Room 5.00,
Baltimore, MD 21201, USA
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Relationships of FFARG and FFARG2 mRWA levels to obesity, diabetes,
and hyporthosolthomia in thesus monkeys
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Enkaryotach Muddid. Objudata, Vertebrata, Mammalla, Butherla,
Primates, Cararkini, Cercepithecidae; Cercepithecinae; Macaca
1 (kases i to 1759)
Hotta.M., Chelafech I A., Veskicka.S., Ortmeyer.H.K., Bodkin.N.L.
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Hotta,K., Gistafson,T.A., Yoshioka,S., Ortmoyer,H.K., Bodkin,N.L.
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Best Local Similarity 100.0%, Fred. No. 2.40c.62,
Matches 29, Conscrativo 0: Mismatches 0; Indels
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/db_mtet-"taxon:9544"
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1. 1759
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Submitted (07-AUG-1995) K.G. Lambe, Zeneca Central Toxicology Lab., Alderley Park, Macclesfield, Cheshire SKIO 411, UK Location/Qualifiers
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Vertebrata; Mammalia: Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                         21-AUG-1997
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/note="alternative start site"
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/db_xref="SPTPEMBL:Q15178"
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/clone_lib="lambda ZAP II"
/clone="CLI5-2a-2"
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/db_xref="taxon:9506"
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Hortack. Pasatson.T.A. Vesbioka.S., Ortmeyer.H.K., Modkin.N.L.
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(Bases 1 to 1765)
Hottark, Prstatson, LA Vesbjeka S Ortmeyer H.R., Podkin, N.
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Schmitted (F6-N-V-1997) Obesity and Diabates Pesearch Center,
Pepaliment of Physiology, University of Maryland, School of
Medicine, 10 South Pine Street, MSIF Room 6-00, Baltumore, MD
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        Similarity 1 (**) Pred. No. 2.4.6-52;
Zimilarity 1 (**) Pred. No. 2.4.6-52;
Zimilarity (*) Mismatches (*)
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/N_Late: "takon:3544"
/Tissue_type "adipose"
/iote "peroxisome"
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Marara malatha
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                                                 ind Hansen, B.C.
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Submitted (19-MAR-1998) P.falciparum Gonome Sequencina Consortium,
The Sanger Centre, Wellcome Trust Gonome Campus Hieston, Cambridge
                                                                                                                                                                                                 1 (bases 1 to 1794)
Hotta, K., Gustafson, T.A., Yoshioka, S., Artharyet, H.K., Budkin, N. L.,
and Hansen, B.C.
                                                                                                                                                                                                                                                                Relationships of PPARgamma and PPARgamma2 mRNA levels to chesity, diabetes and hyperinsulinemia in rhesus monkeys Unpublished
                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 1794)
Hotta, K., Gustafson, T.A., Yoshioka, S., Ortmeyer, H.K., Hodkin, N.L.
and Hansen, B.C.
                                                                                                                                               Bukaryotae: Metazoa; Chordata: Vertebiata: Mammaliu; Buthenia:
Primates: Çatarrhini: Gercopithecidae; Ceregeitherinae: Manaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (06-NOV-1997) Obesity and Diabetes Resenteh Center, Department of Physiology, University of Maryland, Schwed of Medicine, 10 South Pine Street, MSTF Room 6-06, Bullimote, M
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Plasmodium falciparum DNA *** SEQUENCING IN PROSPESS *** 1108
CONTIG 3-59, Complete sequence.
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Pred. No. 7.71e-02;
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(PPARgamma) mRNA, complete cds
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The Tell 18, 1998 this supported on replaced givefid425.

Whishin in a subjective a unimized and live of recessing represent the content of the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E coli, yeast, vector.
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DREIN. I ALGEBERS MALIERA GOLDWIN PNA PROPRESSORE 5 FL CLONG MPP13.
ATTERSION ARRENOTS
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clone:MFB13.
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Embryophyta: Hadbe-phyta: Ared plants: Magnollophyta;
enditodyte-Jans, Rasidan: Capparales: Brassicaceae; Arabidopsis.
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/db_xief="taxon:5833"
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25819 a 14125 c 14111 q 26321 t
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1 (bases 1 to 85)

Keene, J.D., Levine, T. and Gao, F.
Methods and compositions useful in the recognition, busing and methods and compositions useful in the recognition of Thomacieic acids involved in cell growth neophasia and immunoregulation
Patent: US 5525495-A 97 11-JUN-1996;
ACO05170 108056 bp DNA HTG 16-SEP-1998

*** SEQUENCING IN PROSESS *** Arabidabas thathara 'Tama' BAC
'T29E15' genomic sequence near marker Cicoccot : Hids phase 2. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidogsis thailana 'IAMO' BAC 'TD9ELS' gonomin sogrence near
marker 'CICO6CO7'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * This sequence is untinished. It consists of 1 contists for which the order is known. The lengths of the gate fact from * estimated by the submitter but are not known exactly. When * sequencing is complete, the sequence data presented in this * record will be replaced by a single finished sequence * with the same accession number.
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1.6%, Score 28; DB 17: Length 108056:
Best Local Similarity 100.0%; Pred. No. 7.716-02;
Matches 28; Conservative 0; Mismatches 0: Indois 0:
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Rounsley, S.D., Lin, X., Ketchum, K.A., Crosby. M.L.
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Rounsley, S.D. and Lin, X.
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First Submission
Shift of Law AAA. 1998) Institute of Parasitolody, Academy of Sciences of the Czech Republic, Branisovska 31, the Czech Republic Incarfor, Amalitiers
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Direct Submission
Submitted (09-MAY-1947) J.G. Williams, Mrd Laboratory for Mol. deli-
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2 (bases 1 to 1100)
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Capellinn, Tognolli.M., Flach.J., Serrue, 3., reneises, oregin.H.
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Best Local Similarity 100.0%; Prod. No. 2.436-01;
Matches 27, Conservative 0; Mismatches 0; Indels 0; daps
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D.discoldeum mRNA for stat protein, culmination stare.
Y13098
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                 Arabidopsis thaliana
Eukaryotae; mitochondrial eukaryotes; Viridiplantan
                                                       /organism="DictyOstelium discoideum"
Ouery Match 1.5%; Score 26; (B.21); Best Local Similarity 100.0%; Pred, No. 7.526-01; Withhes 26, Conservative 0; Hismathics 2,
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529, 1032
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2 (bases 1 to 1289)
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Simon, P.
Direct Submission
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NOT (1), PHANL SCHOOL PREVIEW NR
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CTABLE ALONG MANATERIANG MANAT
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Submitted (03-APR-1997) Institut de Biotechnologie des Flantes, tar
630, universite Paris XI, Orsay 91405, France
Location/Qualifiers
                                                                                                                                             Nicotians Sylvestris
Eukaryota: Viridiplantare Charephylagintysphyta aroup:
Embryophyta: Tradhoophyta; ouphylagintes: Sjermatephyta;
Marnollophyta: radicopylagos, Asteridae: Selamaner: Selamales:
Solanaceae; Nicotiana
I (bases 1 to 1983)
Lalanne, E., Mathieu, C., Vedel, F. and De Farque, E.
Isolation of two diploid tebusic stands (Arressis), Nos. Treque, 196497) encoding the mitochondrial ATPase beta Land beta 2
subunits (PGP8-163)
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Neopteryafi; Teleostei; Eutelmostei; Amanthopteryafi;
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/db_xref="PID:q3676296"
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1 (bases 1 to 2178)
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Lalanne, E.B.
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2 (bases 1 to 2178)
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(bases 1 to 2482)
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Sequence and devolopmental regulation of the gene that encodes the Secretary discolders 13 ribosomal protein
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Elrect Submission Similarion (2.2-FFP-1998) Toosli F., Institute for Human Genetics, c/o MPI of Blophys. Chem., University of Gottingen, Am Fassberg, Orthingen, 37077, GERMANY
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Find Mil 2,43m-01;
C. Mismatches 0; Tr3414 0;
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2 (bases 1 to 3034)
Wang, X.-Z. and Ron, D.
Direct Submission
Submitted (14-APR-1598) Skirball Institute, New York University
Medical Center, 550 First Ave., New York, NY 10015, USA
Location/Qualifiers
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Wang,X.Z., Kuroda,M., Sck,J., Batchrarora,N., Kimmel,R., Chung,F. Zinszner,H. and Rowla.
Identification of novel stress-induced genes downstream of chop. EMBO J. 17 (13), 3619-3630 (1998).
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Best Local Similarity 100.0%, Pred. No. 7.52e-01;
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/db_xref="taxon:10090"
/cell_line="NIH-3T3"
'db_xref="taxon:44689"
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/Boured "Pibagal76617"
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Firstored M., Coppell K.L., Corroranti M., Foote, S.J., Brown, G.V., Anderskief, and Komp. D.J.,
Stippling of the RESA gene of Plasmodium falciparum
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Best Local Similarity 100.0%, Pred. No. 7.52e-01;
Matches 26, Conservative 0: Mismutches 0: 1.06-38
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Dictyostellum discoldeum DNA, clone app87-;.
Dictyostellum discoldeum
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/codon_start=1
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/db_xref="P1D:d1003589"
/db_xref="P1D:q217302"
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Department of Botany
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Goog sapions transmembrane protein Jagged 1 (HJ1) mRNA, complete
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(bases 1 to 6457)
Lindsell.C.E., Shawber, G.J., Boulter, J and Weinmaster, G. Jagedl. G.E., Shawber, G.J., Boulter, J and Weinmaster, G. Coll. EU (b). 909-917 (1955)
ABSSALGEPERSONPOREDEPERSONANGAASSAASSAAGSTSTST 1593. 1702. 1702. 1701. 1702. 1701. 1703. 1701. 1703. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1704. 1
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/db_xref="taxon:9606"
/chromosome="20"
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Bukaryotae; Mitochondrial eukaryotes; Alveelata, Apicomplexa:
Bukaryotae; Ito 5742)
I (Basea I to 5742)
Murakami.K., Tanabe,K. and Takada.S.
Structure of a Plasmodium yoelii jene-encedad profit homologous to
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U Cell. Sci. 97 (Pt 3), 487*495 (1990)
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QSCIPLLDDGOCFVHEUTGVJECKSSLUGFVRTRGISKSTIGGRANTITTTRKEHSEFFS
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Best Local Similarity 100.0%; Fred. No. 7.52e-01;
Matches 26; Conservative 0; Mismatches 0; Indels 0
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/db_xref="taxon:5861"
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Submitted (31-JUL-1996) M. Aqostoni Carbone. University by Hilano.

Dip. Genetica E Biologia Micrordanismi, Via Genera 26. Milano.

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McLelliorette, F.L. Fatzer E.L. and Aroscok,
Hemiascomycetes; Saccharomyretales: Sarcharomyretariae;
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complement(3002, .4792)
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Rodrigues-Pousada,C., Me
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Direct Submission Submitted (O'FEB-1996) M. Remacha, Centro de Biologia Molecular. Submitted (O'FEB-1996) M. Remacha, Cantoblanco, E-28049 Madrid. Statis (bases 1 to 38516)
Hoffman.L. and Rechsteiner, M. Moffman.L. and Rechsteiner, M. Molecular cloning and expression of submitty of the 265 protessome FEBS Lett. 404 (2-3), 179-184 (1997)
                                                                                                                                                                                    SCCHRIVLA 38516 bp DNA ILK D3 SEP-1997 S. Cerevisiae DNA fragment of 38.5xb iron seft aim of district men 17. x95644
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Saccharomycetaceae; Saccharomyces.
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PHOZ gene, pmtl gene, FMTS gene: QKIl gene: QKIL gene: QRIT gene:
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The sequence of a 16,591 bp segment of Saccharony tes cerevisiae chromosome IV identifies the DUNI, PMII, PMIS, SRP14 and DPR1 yeast 12 (13), 1377-1384 (1996)
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T36742, X04423, X91477, MLINIAL NT9380, NIE4TT, XF1020 125548,
L19169, X2759, L32155, MD2T63, and X76709.
Location/Qualifiers
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/clone_lib="cosmid"
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/translation="WALKEFNDEKENVSLENKHEHINFILE SKINFJWFGVNAFL
IPQSINMAKHUSYAQKASFAARISELLQKHYNYNZWILGHESTVGTDIATIANGK
CARVAKSIGYLAKEFSFILSTNIKKUNASFFUNNKNLLVUHATILSTSSWANIE
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/note="ori, 4"15 ldently with PORI_FEAST PO4840 OHIER
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YQLATOSGWYVRERGNELGGSGCLRIIVGTHEEKTHLIKYFKETLYKLANE"
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/note="orf, len: 209, CAL: U.LU. SIRVIA! "Or protein-tyrosine phosphatases"
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         DNA. Chromosome 4. Pl clone: Mn.114.
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Embryophyta, Tracheophyta, euphyllophytes; Spermatophyta;
Magnoliophyta; eudicotylodoms; Rosidae; Cappatales; Rossieaneae
                                                                                                                   Arabidopsis thaliana (strajusco)umbiu) buka sipops (stembrs); s. e. esse MED14.
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Yasukazu Nakamura, Kazusa DNA Research Instituto, Laboratory of Gene Structure 2: 1532-3, Yana, Kisarazu, Chiba Z'sz. Jafou.
(E-mail:ynakamučkazusa.or.jp, Tel:-81-438-52-4435.
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Dunn, P., Shinn, P., Buchlet, E., Tavarri K., Fridani, Kim, C.,
Walker, M., Comway, A.B., Conway, A.B., Kutzyle, Gillor, Shon, Y. K.,
Toriumi, M., Vysotskala, V., Yuy, G., Tavis, E.W., Trelorspici, N.A.,
Theologis, A. and Ecker, J.R.
Genomic sequence for Arabidopsis Halliana HAY Filans.
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Ecker, J.R.
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Mingall,K., Lawson,D. and Barrell,B.
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gap of unknown length contig of 7180 bp in length.

102377:

95198

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repeat_region
                                        PEFERENCE
AUTHORS
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                                                                                                                                                                                                                                  COMMENT
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Primates dutiling, Foringes Homo,
Primates dutiling, Foringes Homo,
Drimates 1 to 146539)

1 (base 1 to 146539)
Rs Minister Dr. Arrivally Forcum, J., Ganesh, R.,
Ghen, E., Dl.W., Ding, Y., Dundan, S., Durbin, J., Forcum, J., Ganesh, R.,
Garcia, C., Goodman, M., Gorrell, J.H., Haywood, M., Jackson, L.,
Garcia, C., Goodman, M., Gorrell, J.H., Haywood, M., Jackson, L.,
Raskid, M.D., Ergall, S., Principal, P., Lau, R., Leal, B., Liu, W.,
Logan, C., Lu J., Ly, Marther C., Cewal, G., Perer, J.
Raskid, M.D., Ergall, E., Raskind, R., Savage, I., Scherer, S.,
Chinali, C., Nolson, D. and Gibbs, R.A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCIDENT 149538 bp DNA PRI 29-JUI-1908
Home Sapiens 13924 PAC PPCII-46F2 (Poswell Park Cancer Institute
Human PAC ilbrary) complete sequence.
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Mirect Submission
Signified (Mer.May-1009) Milegular and Human Genetics. Boylor
Milegular (Medicing) One Poylor Placa. Houston, IM 77030, USA
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Littled Submission

Littled C. Redictine, One Baylor Plaza, Houston, IX 77030, USA

Collegy K.C.

Direct Submission

Labort Submission

Littled (DT UR1-1999) Milecular and Human Guictios, Baylor

College C. Mcdioxine, One Baylor Plaza, Houston, IX 77030, USA

4 (bases 1 to 149539)
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conting of 5736 bp in length gap of unknown length gap of unknown length lagged of whom length gap of unknown length labbes conting of 41st pp in length latter, conting of 751s lp in length latter, conting of 751s lp in length latter, conting of unknown length latter, conting of unknown length
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Chiu, M.W.
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Homo sapiens
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College of Medicine, One Baylor Plaza, Houston, TX 77230, USA Morley-K.C.

Worley-K.C.

Worley-K.C.

Submitted (28-JUL-1998) Molecular and Human Genetics. Baylor Submitted (28-JUL-1998) Melecular and Human Genetics. Baylor Sollege of Medicine, One Baylor Plaza, Horeron, TX 7030, USA College of Medicine, One Baylor Plaza, Horeron, TX 7030, USA Sequencing is completed to a minimum standard of double strain coverage with a minimum of I clones and 2 reads with no mach grain ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.
                                                                                                                                                                                                                                                                                                                                                                                                         Exon/Intron boundaries of identified genes were chosen if there were canonical splice junctions that maintained sequence continuity across the splice junctions.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                             Sequence similarities were identified using Fowerblast by Jinghil
                                                                                                                                                                                                                                                                                The repeat regions shown were identified using SupeatMasker by
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/clone_lib="Roswell Park Cancer Institute Human PAC
library"
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complement(37. .65)
/rpt_family="(GGA)n"
complement(76%..880)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RPCI1-46F2"
/chromosome="12"
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3179, 327
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complement(3773. .3832)
/rpt_family="L2"
complement(3796. .3871)
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/rpt_family="AluJo"
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/rpt_family="MIR"
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3563, .3654
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7479. .7685
/rpt_family="LIME1"
7740. .8042
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1020. .1057
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complement(6422. .67
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748. .7165
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7166. .7470
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3421. .3479
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/rpt_family="AluSq"

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/ipt_lamily Al_Fibt"
complement(cod14, 16714)
/rpt_lamily Alusx
complement(folls, 1714)
/rpt_lamily Wilmer
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Templement (1253)
Templement (12532, 1260)
Templement (12532, 1260)
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/rpt_lumily "Alusa
/mps.com/(12996, .12748)
/mr.lumily "(GAA)n"
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/rpt_tamminy "Alusq"
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//SEpicecot(16199, 16478)
/pt_tamily "LIM84"
!6284, 16414
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Complement(18923, 18984)
/rpt_tum[]y-"MIR"
1919, 19562
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complement(20237, .2040)
/rg._lamily "MIR"
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complement(19582, 19620)
/rft_family="L2"
pare= 1954
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776 t_lually "(GAAAA) b"
Complement (20450, 120755)
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/*mplowent(22016, .22008)
//or /wmlly "Aluth"
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ZFF_tambly "Aluso"
Complement (8848, 1896
                                                                                                                           " ((P()AA) E."
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14. "Alisk"
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Direct Submission
Submitted (24-SEP-1998) P.falciparum Genome Sequencias Consortium.
The Sanger Centre, Wellcome Trust Genome Campus, Hinston, Cambus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GB10 15A, UK
For more information about this sequence or the Material productive see http://www.sanger.ac.uk/forjets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/Projets/P
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* the sequence data presented in this record will be represent.

*by a single finished sequence with the same accession neather.
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1 (bases 1 to 151018)
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Rest Local Similarity 100.0%; Pred. No. 7.52cm;;
Whiches 26; Conservative 9; Miscatches († 1854)
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complement(25553, .25627)
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ACCESSION

SCR. WYER

REFERENCE ATTHE R. TENRIT

PXEXXCU

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* This sequence is unfinished. It consists of 31 contigs for which the order is not known; their order in this record is a rabitrary. In some cases, the cract longths of the gaps of between the contigs and also unknown; these gaps are presented as as rans of it is a normerism of this record will be replaced the sequence data presented in this record will be replaced to a single finished sequence with the same arression number.

* by a single finished contig of 6349 bp in length

* app of unknown length
                                                                                                                                                                                                                                                                                                                           Epimacher 1 to 186988)

Bymacher Submission Progretto Conway.A.B. and Davis.P.W

Direct Submission 1999, Stanford DNA Sequencing and Technology

Center, Stanford University, 955 California Avenue, Palo Alto, CA
12 PFIACISI genumic sequence: HTGS phase 1, 31 unordered pleces. Acc25505
                                                                                                                HTGS_PHASE:
malaria parasite P falciparum.
non-andium falciparum
Eu; non-andium
Eu; non-and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *** WARMING: Phase 1 High Throughput Genome Sequence ***
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centry of 5445 bp in length
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contra of 16200 bp in length
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* This sequence is unfinished. It consists of 15 contigs for which the order is not known; their order in this receid is arbitrary. In some cases, the exact lengths of the gaps is between the contigs are also unknown; these gaps are presented as runs of N as a convenience only. When sequencing is complete, the sequence data presented in this receid will be regimend by a single finished sequence with the same accession number.

1 2197: contig of 2197 bp in length

2198 2262: gap of unknown length
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Fancy.F., Yingy.F., Pan.H., Dumanski,J. and Roe,B.A.
Direct Submission
Submitted (25.AUG-1998) Department of Chemistry, And Blochemistry.
The University of Oklahoma, 620 Partington Oval, Room 208. Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACOOSE28 183909 bp DNA HTG 27-SEP-1998
*** SEQUENCING IN PROSPESS *** HIGS phase 1, 15 undidered places.
ACOOSE28
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Byroth K. Lincell Fund, E.L., Conway, A.B. and Davis, K.W.
Lincell Solutission
Sidelited (http://org.) Staniord DNA Sequencing and Technology
Conference (http://org.) Staniord University, 855 California Avenue, Palo Alto, CA
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Cirect Submission

Limited Structure 1928) Nematical Sequencing Project, Sanger Centre, Mainten, Johnson Linia, 186 and Lepartment of Jenetics, Manager Centre, Mashington University, St. 19045 MA 67110, 498. E-mails, Sessioner as uk or reineatede wistled with E-mail in the Sequence of Sequence wistled and down for the George of Sequence is no progressed. The Sequence is unfillabled and down for the George in progress and the release of this data is based on the understanding that the Sequence is that it is based on the understanding that the Sequence is that it is the Sequence is in progress on the release of this data is based on the understanding that the Sequence in Manager and Manager is not known; 800 m's separate
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* the sequence data presented in this record will be replaced
*by a single finished sequence with the same accession number.

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Hinxion, Cambridge CP10 (PQ) UK and Pepartonni of Telectics. Nashington Enversity, St. Lovis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rwhnematode.wastl.edu.
jes@sanger.ac.uk or rwhnematode.wastl.edu.
in Oct 5, 1998 this sequence is unfinished and obes not necessarily represent the correct sequence. Nork or the sequence is in progress and the release of this data is based on the sequence is in progress sequence may change as work continues. The sequence may be contaminated with foreign sequence from Ecoli, yeast, vector. Phage els. Order of sequence from Ecoli, yeast, vector.
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Location/Qualifiers

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ACCESSION A1037857
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Tel: (301) 496-1550
Bmail: Robert_Strausbergfaih.gov
This clone is available royalty free through LLNL: contact the
IMAGE Consortium (infolimage.llnl.gov) for further information.
Insert Length: 62 Std Error: 0.00
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High quality segrence strg: 4**
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Initial assessment of human gene diversity and expression patterns based upon PK million nucleotides of CDNA sequence Marine RFT (FRAT Sippl), Fil4 (1945)
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Eucaryotae: Metazoa; Chordata; Vertebrata; Gnatiostometo; Manmedia: Eutheria: Primates; Catarrini: Horlington Home; Home; To 430)
Hillier L. Clark, N. Forbego, T. Fritten, V. Forbins, M., Holman, M., Hultman, M., Kurala, T., Boys, E., Martol, Martol, M., Parsons, J., Rikin, L., Rebling, J., Soares, M., Long, F., Control, C., Con
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This clone is available royally-free through LLNL; contact the IMAGE Consortium (info times) lnl, every for tottler internal learn.
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WashU-Merck EST Project
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Contact: Wilson RK
WashU-Merck EST Project
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1754b04.rl Scares fetal liver spleen INFLS Homo sapiens obnA Glone
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1 (bases 1 to 41)
Hiller, Codal, N., Dubuque, T., Elliston, K., Hawkins M., Holman, M., Hucsba, T., To, M., Lennon, G., Marra, M., Parsons, T., Piffing, T., Tan, F., Irovasis, E., Municislinia, M., Millerinia, M., Millerinia, M., Millerinia, F., Trovasis, E., Municislinia, M., Millerinia, P., Arkisto, F., Topiblished (1995)
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Nashdratus EST Froject
Washbatton University School of McGloine
HA44 Forest Fair Lithkay, F.N. Fl., Ft. 1
Tel: 314-286-1810
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1 (bases 1 to 393)
Hillar.L. Clark.N., Erkoque, T. Filiston K. Harkins.M.,
Holman.M., Hultman.M., Kucako, T. Le.M., Lennon G., Marra.M.,
Parsons, J. Pifkin, L., Pohlifing, T., Soares, M., Tan.F.,
Treyaskis, E., Waterstin, F., Williamson, A., Wohldmann, F. and
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99.0%; Pred. No. 0.00e+00;
ative 0, Mismatches 4,
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pretty p17.54 (Pharmacia) with a modified polylinky host-DH108

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Washington University School of Medirine
4444 Forest Park Parkway, Rox 9501, St. Louis, Meedon
Tel: 314-286-1800
Fax: 314-286-1810
Email: est@watson.wustl.edu
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LOCUS H70160 435 bp mPNA EST 24-OCT DEFINITION 7501510.r1 Home sapiens CDNA clone 213571 5' similar to SP:MEKL_HUMAN P80192 MIXED LINEAGE KINASE 1 :.
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(tuses I to 450)

Olark, M. Debrare T., Elliston F., Hawkins, M., Holman, M., Kucaba, I., Le, M., Lennon, G., Marra, M., Parsons, C., Rikkin, L., Rehiffog, T., Shares, M., Tan, F., Trevaskis, E., Watcraton, P., Williamson, A., Wehidmann, P., and Wilson, R.
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Washo Morek ESI Project
Washogton University School of Medicine
4144 Porcest Pair Pair Pairay, Box 8001, 84, L
fel: 314, 286, 1800
Fax: 314, 286, 1810
Frail: est, waston, wustl, edu
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Deuterostomia: Chordata: Vertebrata, Gnathostomata. Steichthye
Sarcopterygii, Choanata: Tetrapoda: Amniota: Mammalia: Theria:
Eutheria: Archonta: Primates: Catarrhini: Hominidea: Homo.

1 (bases 1 to 407)
11. (bases 1 to 407)
12. (bane, N. Pubuque, T. Elliston, Hawkins, M. Holman, M., Hultman, M., Prokes, T. Elliston, Carrollo, Marra, M., Parkons, J., Pifkin, L., Ruhling, T., Scares, M., Tan, F., Marra, M., Proveskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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Best Local Similarity 98.6%; Prod. Mo. 2.966-299;
Matches 362; Conservative 0; Mismatches 4; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    St Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
444 Forest Park Parkway, Rox A501, St L
Tel: 314 285 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
High quality sequence stops: 273
Source: IMAGE Consortium, LLNL
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and M. Fatima Bonaldo
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Curran close-21457; primer MI4RP; ibbrary-Soars tetal liver spleen
NNIS cover prints (Pharmacia) with a modified polylisher
Extra the (ampletion resistant) NSIA-Pac; PSIA-Fec RI Liver
Fill Spleet form a 2-week-pest curreption mail elets, ist strand
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Hilliar.L. Clark.N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kuraba, T., Lio, M., Lourenco, Martar.R., Parsons, J., Rifkin, L., Rohlfing, Southes, M., 1814, F., Rikhin, L., Rohlfing, Southes, M., 1814, P., Materston, P., Williams, L.A., Wellismin, June
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Local Similarity 98.9%: Pred. No. 1,24e-291;
es 356; Conservation A. W. 1,24e-291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              constructed by Bento Scares and M.Fatima Bonaldo.
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WashIngton University School of Medicine
4444 Forest Park Parkway, Rox 85:1, St. Lonis, Tel. 314, 286, 1800
Fax: 314, 286, 1810
Email: est@watson.wustl.edu
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Keller T.M., Flickhuch, M.M., Pritchman. J.L., Geograph. P. T. M.,

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Relief T.M., Fritchman. M. J. J. M., Shirley. P.,

Small W. V. Spriggs T.A. Miterback T.P., Weidman. J.E., Lily.,

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Shound L. Lil. J.L., Creene. J.M., Gruber, J., Hudson. P., Kim, A.K.,

Korath. R. Weiger T.A. Miterback T. H. Missener P. Kim, A.K.,

Raymond. L. Mel. W. J.S., Greene. J.M., Gruber, J., Hudson. P., Kim, A.K.,

Franker, C.M., Pannon. M.R., Rosen, C.A., Haseltine. W.A., Fleids, C.,

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Franker, C.M., Fannon. M.R., Miller, M. M. Squence

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Mallion, P.C., Sappi), J. T. (1995)
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For clone availability, additional sequence and expression information related to this EST, please check the TiGR Human Gene Inch A. 1973, 1987, 1987, 1981.html)
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Clone distribution: NOI-CRAP Plone distribution information mar be
found through the L.M. A G.E. Consortium/LLNL at:
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Tel: (301) 496-1550
Email: Pobert_Strausberg*nih.gc..
CDNA Library Preparation: M. Bonto Soares, Ph.D., M. Fatima
Donaldo, Ph.D.
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CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Grea Lennon, Ph.D.
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Email: Robert_Strausberg hih.ucv/Tissue Prominement Ciristoffic: M Emmert-Buck, M.D., Ph.D.
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CENALIBRARY Arrayed by: Greg Lennon, Ph.D.

DNA Sequencina by Washington University Geneme Sequencing Center

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format Archard Life I.M.AG.E. Douscortium/ILNE at:
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MILLION BLIGGA, No. 141 (117 MIL perfect)

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Tel: (3.1) 496-1550
Email: Robert_Strausberainih.sov
Email: Robert_Strausberainih.sov
Strausberaini Preparation: M. Bento Soares, Ph.D., M. Patima
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DNA Sequencing by: Washington Citierally Secome Sequencing Tenter
Clone distribution. NCI CGAP clone distribution information can be
found through the I.M A.G.F. Consortiom/LLNL at:
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Eukaryota Metazoa: Chordata Vortebrata, Mandolla, Etilezlar
Frimates: Catarrhini, Hominidae; Homo.
1 (bases 10 490)
NJI-GGAE http://www.n-ki.nlm.nlm.genone Anatomy Project (GGAE)
National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                            268 CIACITGICCIGCALCTICICAAGGATAGGCACAAICATGICAAAITIGGGICGCIIISC 327
                                                                         148 GGCTGGGGTAGTACCATGACTGGAGGGGGGGGGGGGGGAATTABAGGCTGCTGCTTG333 2;7
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/lab_host="SOLR (kanamychn resistant)"
i 132 c 145 g 108 t
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Tel: (301) 496-1550
Email: Pobert_Strausberg bilh gov
Ensue Programment: Toffrey Modelnos, W.D.
Emmert-Buck, M.D., Ph.D.
Best Local Similarity 190.08, Fred. No. 4.216-275;
Matches 253; Conservative 0: Mismatches 0:
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/clone_lib="NCI_CGAP_Kid6"
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[ bases 1.0 499)

#!!!er,L., Altelo.M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.

Kifman,D., Kicaba,T., Lacy,M., Le,N., Lenon,G., Marra,M.,

Martin,J., Korcha,T., Scheltuberg,K., Steptoe,M., Tan,F.,

Incising,R., White,Y., Wylic,T., Materston,R. and Wilson,R.

Kasho McI. Nondan EST Project.
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This clone is available royalty-free through LLNL : contact the
TMANE vonsortium (info-simede-limi.gov) for further intermation.
Pessible reversed clone: similarity on wrong strand
Seq primer: -44ml3 fwd. ET from Amersham
Hish quality sequence stop: 450.
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4444 Forest Park Parkway, Box 9501. St. Louis, MC 63108
4412h | 14.1%) Score 254: DB 14, Dength 490; and Similarity 104.0%; Pred. No. 4.216-275, s. 254: Conservative C. Mismatches O; indexs C.
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CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Grea Lemnon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing fourter
Clone distribution: ACL CGAP clone distribution information can be
found through the I M A G F Des Films, IIML at:
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Primates; Catarrhini: Hominidae; Homo.
1 (bases 1 to 519)
NOT-CGAP http://www.noti.els.abs/noicgap;
National Cancer Institute, Cancer Genome Anatom; Frojest (657AF);
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Fmail: Pobert_Strausberg'hilb.so.
Tissue Procurement Christopher Merkhik, H.B., Ph.B., Michael P. Emmert-Ruck, M.D., Ph.B.
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DEFINITION D182902 cl NCL_CGAP_Br2 Home, Supices that close image 1057202
similar to TP-51148129 of 146129 trenders that EEE ELHARE, a mana
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14.1%: Score 253: DB 11: Legath 499;
Rest Local Similarity 100.0%; Pred. Mo. 4.21c 275;
Matches 253; Conservative 0; Mismatches 0; Indels 1
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Location/Qualifiers
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Tel: (301) 496-1550
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This close is available royalty-free through LINE; contact the IMSE close is available royalty-free through LINE; contact the IMSE close-tilm. (1601ma) tilling of for faither information. Grant Length: 621 Std Broot. 0.00
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This clone is available regalty-free through LDNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reseased clone: similarity on wrong strand INSAT Liength: 1673 Std Error 0 00 Seg primer : 41ml3 fwd. ET from Amersham
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Tel. (301) 496-1550
Email: Robert_Strausbord*nih, gov
                                                                                                                                                Jia (NHGRI)."
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(Joses I to 404)

(1) Conf. Brig. Laws of the Albert Genome Analomy Project (GGAP), Thorse Genome Analomy Project (GGAP), Thorse Genome Analomy Project (GGAP), Thorse Gene Index.
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Best Local Similarity 99.6%, Pred. No. 2.70e-271;
Mat Nos 280, JouserWallive O. Mismatches 1; Indels 0, Saps
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Tel: (30.) 496-1550
Email: Robert_Strausberginin.gov
Tita.c Follocement I. Jeffrey Mcdeires, M.D., Michael
Emmeal.Buck, M.D., Ph.D.
ODWA Library Freguration, David B. Milaman, Ph.D.
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CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Wadlington Tilrowski, morror sequenting Center
Close distribution NII-GRA Proce distribution infiltration can be
found through the I.M A G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                        /organism="Nector: pAMF16, mFNA made from treastve thyroid y under Vector: pAMF16, mFNA made from treastve thyroid younger, cons. made by align-dT priming. Non-directionally element Size-selected to jai v. 30, preside insert size 600 bp. Feference: Rilman - 31 (1946) Cancer Research 55:5380-5383.
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1 (bases Lay)
MCI-CGAP http://www.nchi.nlm.nlb.gov/nchoqap.
National Cancer Institute, Cancer Geneme Anatomy Preject (CCA)
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14.0%: Secre 251: DB 10: Length 404;
Best Local Similarity 100.0%: Fred. No. 1.460-272;
Matches 251: Conservative 0: Mismatches 0: Indels
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Tel: (301) 496-1550
mail: Robert_Strausberginih gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.,
Ph.D., Gerald Marti, M.D.
                                                                                                                                             Insert Length: 621 Std Error 0.00 Seq primer: -40ml3 fwd. EI from Amersham High quality sequence stop. 328.

Location/Qualifiers
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/clone="IMAGE:1133570"
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/tissue_type="thyroid"
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Holt.C.J. Lee, N.H., Kirkoss, F.H., Wellstock, K.H., Franchol, P.C., Manager, H.H., Kirkoss, F.H., Franchol, P.C., Manager, F.H., Caylor, R.A., Cline, T.H., Cotter, M.H., Bulle-Hoddes, H., Fitzbrach, W.H., Fritchen, Bulle-Hoddes, H., Frechen, Goldek, A., Gnehm, C.L., Handan, M.C., Haddelman, N.S., Friedra, M. K., Kalley, J.H., Haddelman, H.H., Fritchen, C. Handles, R.E., McDomaid, L.A., Marganes, E.H., Haddelman, M.S., Fritchen, F.H., Moreno-Palanques, R.E., McDomaid, L.A., Saradak, H.M., Shillips, C.A., Ryder, S.E., Scott, M.L., Saradak, H.M., Shillips, M. Shillips, C.A., Ryder, S.E., Scott, M.L., Saradak, H.M., Shillips, M. Gardarik, D.F., Caol, F., Ferrico, A., Fischer, J., Hastines, J.A., Marke, D., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Greene, J.M., Gruber, J., Hastines, J.A., Frasch, C.M., Mei, Y.F., Wing, J.M., J., H., Meissner, P.S., Greene, J.M., Gruber, J., Hastines, J.A., Finds, M. Frasch, C.M., Marke, M. Willion, P.J., Fannon, M.R., Rosen, C.A., Hastines, M.A., Finds, M., Frasch, C.M., and Venter, J.G., Bussel, G. Handle, G. Hung, G. Groene, G. M., Baschine, W.A., Finds, M., Baschine, M. Baschine, W.A., Finds, M. Baschine, M. Baschine, W. Willion, P.J., Fannon, M.R., Rosen, C.A., Haschine, W.A., Finds, M. Basch, G. Basch
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Enail: atkerlav@tigr.org
Enail: atkerlav@tigr.org
Enc.clone availability, additional sequence and expression
information related to this EST, please clock the TFS Human Sequence (http://www.figr.org.18.572, http://www.figr.org.18.572, html.com
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9712 Medical Center Dilvo, Poscottlo, 18 2 MG 188A
Tel: 3018699056
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Tel: (301) 496-150
Tel: (301) 496-150
Tissue Procurement: Christophur Muskalat, M.D., Ph.D., Michael P.,
Emmert-Buck, M.D., Ph.D.
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Parsons, J., Rufkin, L., Rohlfag, T., Soares, M., Tan, F.,
Tremaskin F., Wolferston, F., Kulling, R., A., Williams, R., A., Williams, R., A., Williams, R., A., Williams, R., R., Manna, R., R., Randerin, F., Wolferston, R., R., Williams, R., A., Williams, R., A., Williams, R., R., Randerin, F., Randerin, R., Randerin, 
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Washir Merre Est Profect
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4444 Forest Park Triber, Professor Contact
Tel: 314 286 1810
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Contact: Pobert Strausberg, Ph.D.
Tel: (301) 46-155

Tel: (302) 46-155

Email: Pobert_Strausberginih.gov

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Emmert-Buck, M.D. Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Meshington, Ph.D.
DNA Sequenting by: Weshington in University Genome Sequenting by: Weshington University Genome Stratibution: No. 25F Fernavrian Things information can be found through the IN A F Converting/Library Arrayed

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Noi-GAB http://www.nutlinih.ga//foriegap.
National Cancer Institute, Gander Gengem Anatoms Frejert (CARP).
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(Holman, M., Far, N., Dubuque, I., Elliston, K., Hankins, M., Helman, M., Hollman, M., Kuraba, T., Le, M., Lebron, S., Marra, M., Fiscos, C., Estan, P., Frengas, C., Fiscos, C., Milling, C., Can, P., Trengas, C., C., Con, C., Con, C., Con, C., Can, C
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DNA Sequencing by: Washington University Genome Sequencing Period
Clone distribution: NCI-CGAP clone distribution information can be
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Tel: (301) 496-1550
Email: Robert_Strausberg/hib.gov
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db_xref="Attoc (inhost) 85996"

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db_xref="Attoc (inhost) 85998"

db_xref="Attoc (inhost) 86991"

db_xref="Attoc (inhost) 86994"

db_xref="Attoc (inhost) 86994"
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14.77 ERYERGEGTÄJFARVATGANTGANGGREGGGANGGGÄNGGÄÄNGGÄÄNGGTGTTTGGGG 1574
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CDNA Library Arrayed by: Greq Lennon, Ph.D.
DNA Sequencing by: Washington University Gurome Sequencing fonter
Clone distribution: NCI-CGAP clone distribution information can be
www-big link-gov/bbreyimage/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Official APP
                                                                                                                                                               1 (bases 1 to 366)
NOT-Gabb http://www.n.pb/nom.nlp.nov.nrieday.
National Cancer Institute, Cancer General Arstemy Project (COAP), Unpublished (1997)
AA772212 366 bp mRNA EST 24.3AM-1998
ai41a03.si Scares parathyroid tumor NbHPA Rome explore to the classical and established to the citable of adjating the transfer.
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Primates, Catarrhini, Heminidae, Homo.
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(Pharmacia) with a modified polyticker; Site 1: Not 1;
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oligo(dI) primer
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/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
1 C 106 q 89 t
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Tel: (301) 496-1550
Email: Robert Strausborgan:
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/clone="1359532"
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Hilleri, Clark N. Puhngoot, Elliston, E. Hawkins, M. Holleri, Clark N. Mucadot, Elliston, E. Hawkins, M. Holman, M., Malthan, M., Marra, M., Parsons, J., Rohlfing, I., Soares, M., Tan, E., Materston, R., Millamson, A., Wohldmann, P. and
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Hish quality sepaery stors, 312
Source: MAGE Consortium, LINL
This close is analisty revelly free through II'NI i contact the
IMAGE Consortium (infolmate illuligov) for further information.
Location/Qualifiers
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Washirwerch FST Project
Washirwerch Dirersity School of Medicine
4444 Forest Park Farkway, Box 8501, St. Lewis, MC 63108
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Editaryolae) Metazca, Eunclasca, Enlateria, Collomata; Deuterostomia; Chordala, Vertebiata, Gnathostomiai, Dividibles; Saropterrygii; Choanara, Terraferia, Annicia, Mammalia; Theria; Eutheria; Archorta; Frinates; Caturthin; Monicidae; Home. 1 (bases 1 to 280)
2 (budgue, T. Elliston, R., Hawkins, M., Hollman, M., Hultman, M., Redaja, T., Elliston, R., Hawkins, M., Farsons, J., Pifkin, L., Pehiliamson, G., Maria, M., Terraskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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Fossible reversed close; similarity on wrong strand.
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y185hil ri Homo sapiens obna clone 45222 5' similar to SP-ANK_HUMAN Q01485 ANKYPIN, BPAIN VAPIANI 2 :. q868797
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Bost Local Similarity 94.4%, Fred My 4 vversof;
Matches 253; Conservative O. Mismatches 15, Indels C. Saps
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Fax: 314 286 1810
Email: est@watson.wustl.edu
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69 c
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Source 120562 primer Promega -11ml3 library-Source retina N244R vector-p1713D (Pharmacia) with a medified polytinker best-balle (ampicillin resistant) Rsitel-Not I Rsite2-Eco RI 1st strand cONA was primed with a Not I - oligo(d) primer of cond was primed and I - oligo(d) primer of conditional 
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Peuterostomia: Chordata: Vertebrata, Gnathosforata: Osteichthyes;
Sarcoperiyali; Choanata: Tetrapoda: Amniota: Mammalia: Theria:
Eriheria: Archonta: Primates: Catarrhini; Hominidae: Homo.
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL: contact the
IMAGE Consortium (into-umare, link, ago) for fullier intormation.
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Hiller, L., Clark, M., Dukaque, T., Eliiston, K., Hawkins, M.,
Holman, M., Fritman, M., Kucaka, T., Le, M., Lennon, G., Marra, M.
Forsons, L., Rifkin, L., Rohlfing, L., Soares, M., Tan, F.,
Crovaskis, E., Katerston, R., Williamson, A., Wohldmann, P., and
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Hessi Certi Similarity 99,6%: Pred. No. 4.096-237;
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                                                                 THE TOTANIATORANG SANAGAGACCTOST 515
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The WashG-Merck Est Project
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WashJ-Morek EST Project
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Fax: 414 286 1810
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Eukaryotae, Metazoa, Eumetazoa, Bilateria, Confomuta;
Deuteroslomia, Chordata, Vertebrata, Guaflostomuta; estejebiliyes;
Sarcopterygii, Cheanata, Tefrapoda; Amniota; Mammalia; Theria;
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Hiller, L., Clark, N., Dubono, T., Ellistop, V., Hacking, M.,
Holman, M., Hultman, M., Kucabo, T., Lo, M., Longon, C., Mara, M.,
Fursons, J., Rifkin, L., Rohlfing, T., Scatter, M., Tun, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wolldmann, F., and
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                                                                                                            yj22d06.rl Homo sapiens chwa cione 149483 similar to
SP.Wik2_HUWAN Q02779 MIXED LINEAGE ELMASE 2 ;
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                  305 AGGGTCTTCATGCAGATCTTCATGAGCTTAMACAMATGAG 448
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WashU-Merck EST Project
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Fax: 314 286 1810
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61 ABDODOGAAGCICIGCASAAGAAGDIGAAGACACAAACAGAGGGGGGGAGGGAGAGAGATSTS 12
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No. I - oligo(dT) primer [5].

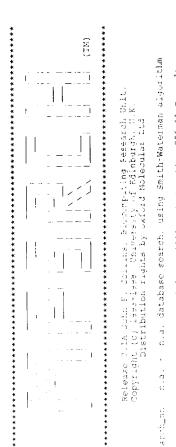
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Hiller..., Clark.N. Elkaya: Eliztu: F. Backin: M. Hallar... Grathus: M. Belman.M. Hultar.N. Eschin: H. Belman.M. Hiltar.N. Eschin: M. Farson: S. Marra.M. Parson: M. Jan.F. P
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Pest Lors' Similarity 100.09; Fred. No. 7.498-276;
Matches 222; Conservative 0, Mismatoles 0;
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Washington University School of Medicine
444 Forest Park Parkway, Pex 9001, 91 11 11: 314 286 1800
Fax: 314 286 1810
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Washi-Morok EST Project
Wishington Talvorsity School of Medicine
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Variance 3.564; scale 2.284 Medi. 8.140; 8.01.81.08 Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Claim 2: Page II: TSpp: Bnglish.

The sequence is an example of their can be from 2 to 50 T's in the mover for use in the invention. There can be from 2 to 50 T's in the loop region. A probe sequence is ligated to the 3 end of the promoter region. Open hyprilation of the probe to a target sequence promoter region. Open hyprilations of the probe to a target sequence and ligation of the hybridised target sequence can be transcribed by maligheliarization of the soften and incorming sequence, the target sequence can be transcribed by
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And backet plage. This Sect B-1 Fits polymorphe:
target sequence amplification; ss.
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011764:
22-011-1991 (first entry)
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11-MAN-1992; 081075;
11-MAY-1992; US-881075;
15-8EP-1993; US-120827;
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New Secreted proteins encoded clones present in ANU 2026.

New Secreted proteins encoded clones present in ANU 2026.

New Secreted proteins cell proliferation/differentiation

requiating, manumodulating and many other activities

claim 9. Page 76-77: 139pp; English man secreted protein deposited

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                                                                                                      Length 98;
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Jacobs K, Lavailie ER, McCoy JM, Merberg D, Racie LA, Spaulding V;
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Hyman secreted protein AM931 encooing CDNA.
Hyman, secreted protein, AF142; AICC 96226; cytorine:
Coll proliferation; differentiation; regulation ds.
Homo sapiens
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V<u>0</u>2135 standard; cDNA; 867 BP.
V02135;
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P-PSDB; W44075.
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1916-957
1908-31 Indels 9
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(15%) Score 26, DB 39, Length 867,

(1) Similarity 45,4%, Bred. No. 7,006-15,

(2) Tokenthalice () Mismatches I: Inde)s
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Ential of MA elone encoding secreted protein AM931.
By a servered protein research treatment AM931.
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M. Marian Control of Contro
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23-MAY-1996 (lirst entry)
Full length cocont LPAM clone order,
Evolussabatide acid acyl transforaso; everymer; meabatide acid acyl transforaso; everymer; meabatide acid acyl transforaso; everymer,
I acyl dlycerol.3.phosphate acyl transforaso; acyl eva forms; primer;
Probe: blotechnology, medification; trinspectide; anglibication; ss.
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Zeamatin cDNA may be obtained using standard bNA techniques, and may be expressed under the control of the constitutive 45s promoting transgenic plants - plants expression high zeamatin, levels large contained resistance to plant pathoders. Seamatin, levels large synergistic antifungal proteins (SAFPS), synergise with other antibotics such as nikkomycin. Alone, they display tunoloide activity against fungi including Newpospera and Interpretation.
                                                                                                                                                                                                                                                                                                                                                                                                           ENA encoding Synergistic Anti-Fundal Profein - obtained from cotto, sorghum and oat, used in synergistic compsus, against find i and yeasts, e.g. Neurospora and Candida.
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N.B. On decoding this cDNA sequence, the complete remarks profess.

Sequence given in SEQ ID NO.4 is not obtained.

Sequence 894 HP. 185 A: 287 C: 277 C: 144 T:
                                                                                                                        19..21
/*tag* a
/note* "star: cub n 10: Pound: n. Cudina sepanae"
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12-FEB-1996 (first entry)
Zeamatin synergistic antifungal protein ending segments.
Zeamatin, synergistic antifungal protein; fungicide; pesticide; transgenic plant; disease-resistance; ss.
                                                                                                                                                                             62.84
/*tag- b
/mote= "first codom of meture reamatin prefeit."
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Best Local Similarity 100:08; Fred. No. 7.000-05;
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259..1182
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T08171;
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09 JAN-1995; U00432,
10.JAN-1994; US-178708,
(CIRB.) CIBA GEIGY AG.
(UYRE-) UNIV RES CORP.
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06-APP-1994; US-224625.
21-APR-1994; US-231196.
06-UIN-1994; US-254404.
21-GIT-1994; US-327451.
(CALJ ) CALGENE INC.
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F.FSDB, R75930.
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WPI; 95-366394/4
P-PSDB; R87723
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WPI; 95-06
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                      Example 3: Fig 13: 127pp; English.

According to the planting and any transferance (LPART ESTIGAT) mined from the planting and any transferance (ASSPAT) from concount or recommend to the characteristics of Reed (ASSPAT) from concount or mondowncount bare the characteristics of Reed from cytophasmic montroller the plant. Any profession of the plant, have prefer a strainful the peptide sequences RETOINT. The peptide sequences were used to design only observed and meadowfrom condomination of AGSPAT clones from occount and meadowfrom conditioned in the recorder section with blockedhological applications such as modification of plant grant compens.
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The nettence encodes a grotein of 308 amino acid with a calculated mol.
The nettence encodes a grotein of 308 amino acid with a calculated mol.
SOS-AOB). The protein has a calculated pr of 9.79. The gene was lablated from a occount endusterm CDNA library using probes derived from amino acid sequencing of the protein such as TO8157-8 or using PCR sequence 1408 PP. 372 And 212 C. 321 G. 401 I;
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011711:
(4) 1711-1911 (first entry)

Riman alphanintsicron receptor grotein enoughing sequence
than alphanintsicron receptor untilitat, and tumbot agent,
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Best Local Similarity 180,0%; Pred, No. 7,000-05;
Matches Local Schools of Mismatches Construction Constructi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U42769 standard, cDNA, 1562 BP.
U42769:
U42869:
U43869:
U4386 (first entry)
U4386 induced deck. close 1A8-17.
U4386 induced deck. close 1A8-17.
U50 Ending, library, receptor, growth phase transfittion, richal expansion; ss.
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20-NOV-1991; US-796066.
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Wie310230-A.
IT-MAY-1992.
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UPI, 90-19
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This sequence encodes a recombinant human alpha interferon (IFN) receptor protein useful for the testing of IFN agonists and for treatment and diagnosis of Viral diseases and transurs. Antibodies raised against this protein can be used for blocking the receptor when required, e.g. where overexpression of alpha IFN is harmful. The Abs are also useful for e.g. dup targetting. Variants of the protein, having residue [64 (IAT) Problem 20 August 2
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//abel= glycosylation site
1687..1695
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20-OCT-1989; FP-013770
(GNPS ) CNPS CENT NAT PECH SCI.
(GNPS ) L. URE G. Lutfalla G. Gresser I;
WEI. 9-14874,20.
P-PSDB; R11958.
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/label= glycosylation site
1015..1023
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/label= glycosylation site
1018..1026
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/label= glycosylation site
1204..1212
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/label= glycosylation site
1375..1383
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/label= glycosylation site
1630..1638
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/label- glycosylation site
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338..847
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/label* glycosylation site
250..258
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/label= glycosylation site
319..327
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/label= glycosylation site
340..348
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/label= glycosylation site
106..414
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/label= glycosylation site
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                                                                                                                             /*tag= a
/product= human alpha IFN
79..159
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/product= signal peptide
                                                                               Location/Qualifiers 79..1752
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drug targetting; ss.
Himo sapiens.
Key Local
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02-MAY-1991.
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Fig. (first outry)

P. Labriparum liver state antiden-3 denomic sequence.

P. Labriparum liver state antiden-3 denomic sequence.

Fig. 1845 | Marchiparum pre-crythrocytes from stage antidens serum.

Fig. 1851 | Harrist Labria and the endaminant for exeminations hydrophobics.

Fig. 1851 | Harrist Labria Labria antidens anchoring sequence, antibody;

Fig. 1852 | Fig. 1853 | Marchiparum anchoring sequence, antibody;

Fig. 1853 | Fig. 1853 | Marchiparum anchoring sequence, antibody;
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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N. 172 
L4 ATT 100 (Lits) outry)
Sequence encoding the time-infected Erythrocyte Surface Antiqon
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Local Similarity 100.0%; Prof. No. 7,000-00;
Nos. 25; Conservative 0; Mismatches 0; DD-18
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WPI: 97-034369/03.
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WPI. 97-284-569/53.
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DNA sequences representing aberrant forms of human high mobility group protein genes - useful for treatment of endometriosis and group protein genes - useful for treatment of endometriosis and tumours, or for modulating vascularisation, etc claim: Fig 13, 58pp German.

Py Claim: Fig 13, 58pp German.

Cy Vor80-VO288 are cDNA sequences that connote aberrant forms of the human high mobility group protein (HMG) gene, HMGI-C, which is located on conformation product but not the protein binding denial. These sequences encode the DNA binding part of the cranslation product but not the protein binding denial. Such HMGI-C, protein can be used in Kits to modulate vascularization and this can reduce ablock or stimulate angloses and reported on the proteins of the car improve vascular provision in myocardium damaged by infarction. Such Contraction (local or or all and for tissue responsable) in degenerating or damaged tissue. The responsable can be applied to the carrently impression method can be applied to use up to local or or all value and method can be applied to use up to locate the carrently impressive responsable in another analyzabacit shock, is avoid all 13 % 119 % 12 % 13
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V02896-V02898 are cDNA sequences that encode aberrant forms of the fundamental mobility group protein (HMS) gene, which is located on chromosome 12. These sequences encode the DNA binding part of the translation product but not the protein binding domain. These proteins antibodies derived from these proteins or expression modulators of the
                                          08-MAY-1998 (first entry)
Human HMGI-C aborrant form 13.
High mobility group protein; HMGI-C; MAG; Numan; treatment; modulator;
multiple tumour aberration growth grow; varioular derelopment;
anglogenesis; vascularisation — relometrics; contraception
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Human HWGI-C aberrant form 2

High nobility group protein; HMGI-C, MAG, human, treatment; momulatiple tumour aberration growth gene, mershar development; anglogenesis; nascularisation websmctinesis; contraception
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Olgonucleotides corresp. to the partial sequence of insecticibility protein FLL376 were used as primers for leveraging score in the partial protein FLL376 were used to transform E. english sequence into pks and used to transform E. english score FLL-755 encoded a 249-amino acid protein (aiven, in 87-79.) that from become a precursor of FLL-376. Expression of such proteins endiffrom becomeously vectors is used for biological control of sequence 94, RPP. 322 A; 172 C, 194-61.
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07-JUL-1994; U07595.
07-JUL-1993; US-089998.
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                                                                                                                                                                                                                               W09501996-A
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       Discissive, Fagus 20124, 45pp. English.

Discissive, Fagus 20124, 45pp. English.

This count sequence untiles a north himton Mails scavenger receptiff

(Billian Land). This purpletical and restaining antibodies can be used to recent and cerebral infarction, angina, organ failure, stroke, and and less of Landining They extremities. They are also seed to another, and less of Landining They extremities and other immune cell related host defense discusses a steple shock, penetratiffs, multiple organ and up to be used to treat they bacterial and other and antagonists may also be used to reat they becaused. The polymorphists and antagonists may also be used to remain of Hamioush allowed the because of a discase (or succeptibility to a discase)

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297623.
18-2AN 1956 (filst entry)
18-2AN 1956 (filst protein (CF):1 CDNA.
18-2AN 1956 (Filst ST):2. Little Lisks, Isteppetrusis, Lone morphogum)
18-04000 (filst):2. Little Lisks, Isteppetrusis, Lone morphogum)
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14-FEB-1997 US-794795.
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HUMBAN MARKO CARROTTEL LUCKFULL TO SEA TO GEVELOP FROGUSTS FOR THE WARREN THE CAROOK, bactorial treating e.g. Catliovascular disorders, septic chock, bactorial
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Best Local Similarity 100.0%: Pred. No. 3.50e-04;
Hatches 25: Conservative 0. Mismatches 0; Indels 0
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CHIL-) CHILDRENS MEDICAL CENT.
CATTE HW. CARAJAAR E. FORCAGE A. FLAGERAS A. SOMETS M.
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Thran marcusk cDNA 1.
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26-MAY-1995.
16-NPV-1994: 013215.
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20-MAY 1998
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Identifying opds. that can induce bone formation - from their effect protein of OP-1 protein or its related mRNA, potentially useful protein or its related mRNA, potentially useful protein of OP-1 protein or its related mRNA, potentially useful protein of OP-1 is bisclosure; Page 32-34: 53pp; English.

5 Disclosure; Page 32-34: 53pp; English.

5 Disclosure; Page 32-34: 53pp; English.

6 This sequence represents murline osterogenic protein (CF):1 CDNA. OP-1 is not the pro-domain and one thin of this sequence. From incleolides of the pro-domain and one thin of this sequence. From incleolides of the problem one detect OP-1 mPNA expression. Using this probe sequence of the detect oP-1 mPNA expression. Using this probe sequence of and monoclonal antibodies, it is possible to identify substances that are capable of inducing bone formation by determining that is effect to 15-1 can make expression. Compounds identified in the capable of inducing home formation by determining that are identified in the bone disease, osp. osteoporosis. Compounds that are identified in the capable rapid and sensitive valuetion of candidate compounds. Has it can provide rapid and sensitive valuetion of candidate compounds. Has it can provide rapid and sensitive valuetion of candidate compounds. Also considered within the stype of the production and open that it determent of osteoper production of candidate compounds. Secuence 1872 BP; 433 A; 591 C; 501 G; 347 I:
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Prod No 3.50e-04;
O; Mismatches O: Indels O
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Matches 25; Conservative 0; Mismatches 0; Indels 0
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12442 standard; DNA; 1872 PF
133442;
21-NOV-1996 (first entry)
Mouse estecgenic protein OP-1 cDNA.
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morphogenesis; edentoblast; OP-1; ss.
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14-FEB-1996; UC2169.
1-MAR-1995; US-396930.
(CFBA-) CPEATIVE BIOMOLECULES INC.
Charetto MF, Pitherford PB;
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US-621486.
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C: Caps

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Screening ordes, to determine ability to morphogon, proceeding orders, to determine ability to morphogon, by assaying test tissue type only it judicative of a prodn. level change of morphogon; it judicative of a prodn. level change of morphogon; prodn. level change of morphogon is nactive when reduced but is active as an embryo. This morphogon is lactive when combination with other oxidised in combination with other oxidised in combination with other oxidised homodimer and when oxidised in combination with other of prodning the morphogons are capable of slimitarion of prodning of prodning the proliferation of differentiation of prodning the arowth an amintenance of differentiation of these including the rodifferentiation of transformed cells. These morphogons may also be capable of induction redifferentiation of sequence 1873 BP; 435 A; 589 C; 469 G; 460 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y.
11.7.
                                                                  Morphogen mopl coding sequence.
Morphogen; homodimer; stimulate; projiteration; propert; proping differentiation; growth; redifferentiation; transformation; human; mouse; Drosophila; Menopus; committed cells; hippocampus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Compans. for increasing progenitor cell population - contain a morphogen to induce proliferation, useful for inhibiting neoplastic growth, inducing tissue repair and in diamosts of tissue dystunction.

Nivolecure: Page 98-120 132pp: Fralish.

Mature mOP1 is one of the preferred known morphosures which can be
                                                                                                                                                                                                                                                                       30-AUG-1991; US-752861
(CREA-) CREATIVE BIOMOLECULES INC.
COMER CN. KUBErasampath I, Oppermann H. WKAYRIK E. FILM FHIII
Rueger DC, Smart JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAR-1992; U01968.
11-MAR-1991; US-567274.
(CRFA-) CPEATIVE RIOMOLECULES INC.
COhen CM, Kubersampath T, Opportmann H, Fand FHL. France Let.
WPI: 92-331475/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 1.4%; Score 25; DB 6; Length 1873; Local Similarity 100.0%; Pred. No. 3.50e-64; los 25; Conservative 0; Mismutches 7; 1.56.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3. Made 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine osteogenic protein mOP1 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0: Mismatches
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Mus musculus.
                                                                                                                                                                  Location/Qualifiers
104..1396
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104..1396
LT 23
038858 standard; cDNA; 1873 HP.
038858;
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O2H736 standard+ cDNA; 1873 FF.
                                                 3-JUL-1993 (first entry)
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28-AHG-1992. UOT359.
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P-PSDB; R27290
                                                                                                                                             Mus musculus
                                                                                                                                                                                                                    W09305172-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Onery Match
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RESULT
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used in the manufacture of pharmaceuticals for inducing mon-
chookboard nationalization lists of justifier [projection of produced to the pharmaceution and formula the pharmaceutic control of lifetimization of los marmal. Mirrhogene shalling at least 178 howevery with mop! are locally in a marmal. Mirrhogene shalling at least 178 formula of the mop! are locally of this coding sequence was sequence 1873 BP. 475 A. 586 C. 502 G. 250 I)
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                                                                                                                                                                                                                                                                           Coory March
Sest Local Similarity 100.0%, Fred. No. 3.50e-04;
Marches 25, Conservative 0, Mismatches 0, Indels
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[The Construction of the Construc
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Rueger DC, Smart JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W.745642-A.
3: MAR-1594, C08885.
15.8EP-1993, US-945286.
17.MAR-1993, US-029335.
3: MAR-1993, US-029335.
4.(C1EA-) CREATUVE BIOMOLECULES INC.
Charolte MF, Cohen CM, Kubersempat, Charolte MF, Cohen CM, Rubersempat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1836 atuaaaaaaaaaaaaaaaaaaaaaa 1860
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104..1396
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10 067311 standard, IMB, 1873 PE
NO 067312;
OT 11-701-1994 (First entry)
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/label oF-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -OCT-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI: 94-118121/14.
P-PSDB: R50199.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (表現の最近日の中国に対象と、 ユー・・・・。(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(また)(ま
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/note= "encodes pro protein which when cleaved yields
/note= mature, morghogenically atting pations a
277..1393
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Human esteógenic protein, GF - GF - Margh-Ggen, morph-Ggen, morph-Ggen, morph-Ggenic protein:
embry-ogenesis: organ maintenánce; tissue-specific morph-Ggenesis:
arthilis, emphysoma, osteoperrosis, dirilosis, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Gaps
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Mithographing as implanted tools in 1011, society: 1 initial tissue loss associated with particulated discuss to initial tissue loss associated with particulated discuss or injury older 29, Fage 91-94, 100pp, English.

Mathogens comprising an amino acid sequence sharing at least 00 for innequality with OF-1, CPR-1, CPR-1, VIC. With BMP2(fx), 604(fx) and at least 90% homology with BMP2(fx).

BMP5(fx) and BMP6(fx) are useful for integrating an implanted with periodonal discuss or injury.

Sequence 1873 BP, 435 A, 587 C, 502 C, 349 T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Screening for compounds which modulate merphogen expression - by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
1.4%; Score 25: DB 10: Length 1873;
Best Local Similarity 100.0%; Pred. No. 3.50e-04;
Matches 25; Conservative 0; Mismatches 0; Indels 0
Murine OP-1.

DF-1, DF-2, CBMD2, V31(fx), V31(fx), EDE(fx);

GDF-1(fx), 60A(fx); BMP3(fx), BMD5(fx), BMD6(fx);

LIGELS SORREY, ATTROPLES, DSECURATION, FRICAGE, GARPHOPER, BATTROPLES, DSECURATION, GARPHOPER, DOOR Implement Properties of Friedment, Integration, Editablication, SS.

Mus. musculus.
                                                                                                                                                                                                                                                                                                                                                                                              31-MAP-1994
15-SEP-1993; U08-045285
15-SEP-1993; US-045285
04-MAR-1993; US-029335
31-MAR-1999; US-020335
31-MAR-1993; US-060310
(CPR-) CPEATIVE BIOMOLECULES INC.
Cohen CM, Rukerasampath I, Optermain H. CP
Pang RHL, Rueger DC, Smart JE:
WPI: 94-118107/14
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Cohen CM. Kuberasampath I. Oppermann
PRI, Rueger DC, Smart JE;
WELL 37-38466,35
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104..1396
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/label= 0P-1
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30-AUG-1991; US-752764.
30-AUG-1991; US-752861.
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20-JUL-1994; 278729.
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P-PSDB: W36854.
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This work is not seen that demonstrated coll toxin ethanol Firkhisons, for the demonstrated mayoutcophic lateral solutions.

Firth a selection is neophastic losion control nervous system; CNS; for the selection respirate involusing redifferentiation herroblastoma; for the selection system; by the selection system; system; by the selection association; association as a section of the selection is selected.
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Mid Schollering 1010/%, Prod. No. 4.5 ov. 4.4.

Mishardino. Mishardino. Mishardinos 0; Indels 0; Gaps.
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consists.
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Pischosure: Page 127-129; 176pp: English.

This sequence encodes the murine derived protein, estreanning.

This sequence encodes the murine derived protein, estreanning.

Institute of the mature of protein streams and the protein as the protein of improving survival or instituted.

The mechanical injury, or, 'ransor'ed have settlered as the character of cells exposed to toxins series and Alcheimers discussed because of neuropathies (such as the britanders of streams of the cells amylotical and religious and Alcheimers discussed because of neuropathies (such as the britanders of streams). At this cells cannot be in the cells to the cells of a final cell neoplasms). At this cells cannot be in the cells to the cells of a final cell neoplasms.

The peripheral nervous systems. When used to finite rediction of a final cell neoplasms and the cells are used to treat neuropathias and the cells cannot be requered over long distances. Can be requenced over long distances, can predict the cells of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse esteogenic protein 1 (m.M-1) armo.
Mouse esteogenic protein 1 (m.M-1) armo.
Mouse increase: fracture: prest-meropausal; sending
Bone: loss: increase: fracture: sending in migrostroments; hyperparathyroidism: sending in migrostroments;
where renal fallure: Maney disease; esteomalaria, vitamin; hy
deficiency-induced usteopenia, osteoporosis; Paner's disease;
bone mass; imbalance; resorption; formation; dialysis; calcium;
phosphate; metabolism: murine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hyperparathyroidism and Paget's disease. The methods can be used to:
Protecting individuals at risk for loss of bone mass such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        postmenopausal females, aged individuals and individuals underpointed dialysis. The loss of bone mass may result from an indudence in pencerescoption or bone formation, an imbalance of valcium or the splate metabolism, a vitamin D imbalance of the putility of individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence is that encoding mouse estrogenic protein; (men-1) a a merphogenically active protein which may be used as part of a method for treating a bone fracture or a disease which causes or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    results in bone fractures or other detects in skeletal microstructure. Such diseases include chronic roum; tallure and other kidney diseases, osteomalacia, vitamin D definiency; indired osteopenia or osteoperosis, postmenopausal or semile estemporasis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use of morphogenic or in-vivo morphodenic-stimulation adent to present bone loss or increase, used for treating bone tracting post-memopausal or semile osteopolosis, hyperparathyroidism etc. Disclosure, Page 110-113; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 4%; Scoro 25; DR 10; Labita 1873;
larity 100:0%; Pred. No. 3.50e-04;
Conservative 0: Mismatches 0; Indels
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30-AUG-1991; US-752764.
30-AUG-1991; US-752857.
30-AUG-1991; US-752861.
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WPI: 93-117208/14.
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501 G;
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Cours WE. Faker stratulit. Offermand H. C

Stroger DC. Tucker PF. Cohen CM. Pang RHL:

WPI: 94-365304/08
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Sequence 1873 BP:
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Maridae.
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Freatment of chronic renal failure - using an osteogenic protein/bone morphogenetic protein renal thorapoutic agent or protein/bone morphogenetic protein renal thorapoutic agent or renal mesenchymal progenitor cells userlosure: Page 57-59; ll3pp; English.

This cDNA sequence encodes the mouse osteogenic protein, OP 1. This protein is used in a method for the treatment of a mammal haring or at risk of, chronic renal failure which compress administering or at otherwhole genetic protein (UPJEMP) renal or obtained failure with compression or the method can be used for treatling e.g. thermic renal failure, end-stage in a disease, chronic renal failure, end-stage in disease, chronic renal failure, end-stage in disease, chronic nephrotein, diabetic glomerulegathy, diabetic renal hyperthology in a patient of morphogenesis, hyperthesis or a patient affined with e.g. glomerules in the intending patients of diomeruloscierosis, tubulointersitial sciences of the renal librosis. Such therefore agents can present, thill the distribution agents can present, thill the distribution agents can present the progressive deviation to the need for intended for
                                                                                                                                                                                                                                                                                                                                                                                                                                A hybridisation probe specific to the Constminus of the ENK encoding human (B1 was prepared (base pairs 10%4/15% of 10%4518). The ENK encoding thoman (B1 was prepared (base pairs 10%4/15% of 10%4518). The clabelled probe was used to screen ca. Pour over propages of an order of times 17.5 days p.c. mouse entry 5° structh CNA 411 100 10% of the confidence of the Streething of Structh CNA 411 100 10% of the confidence of the DNA was subcloned and sequenced. Two different DNA sequences were identified; mopel and mopel (mopel is not assembled in this patent specification). The mobil DNA course for
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                                                                                                                                                                                                                                                                                         Osteogenic polypeptides capable of inducing endochondral bone formation - useful for bone and cartilage repair, treatment of osteoarthritis and correction of skeletal and dental
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Best Loral Similarity 100 0%; Pred No. 3 50e-04;
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06-MAY-1997: U07816.

06-MAY-1996; US-643321.

CERA-) CPBAILVE BIOMOLECULES INC.

COHEN CM, SAMPATH KT;

WPI: 97-558690/51.
                                                                                                                                              (CREA-) CREATIVE BIOMOLECULES INC
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V10346 standard; DNA; 1873 BF.
V10346;
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                                                                                                                                                                                 Oppermann H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUN-1998 (first entry)
                                                                     18-0CT-1991; U07654.
18-0CT-1990; US-600024.
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WPI; 92-157101/20.
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W09207004-A.
                                          30-APR-1992
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Arthitiques (ALEMKE) (MA.)
Brythitiques Ext. plant, south Prosecuto plant, AthxXI; untisense,
Trp pield; plant, characteristic, ds.
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.50e-04;
.hee 0; Indels 0;
                                                                           Length 1873;
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                                                            Matrix States 1.4%; Score 25; DB 39; Length 187 Mail Similarity 100,0%; Pred. No. 3.50e-94; S. 25; Conservative 0; Mismatches 0; Indeis
                                    501 G;
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                                587 C;
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/product= ACC_systhase
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Possi replacement therapy.
So pende 1071 Sp. 435 A.
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Vistals
Vistan lass (lirst enery)
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/freedor* ;
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PSIB: W45453.
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DNA encoding anti-sense RNA blocking plant APT Synthase expression of succession and columns 63-68. 91pp. Endish, the delayed trait ripering Example 3; Columns 63-68. 91pp. Endish.

The present sequence encodes tomato
The present sequence encodes tomato
I aminocyclopropanel-carboxylic acid / Arch synthases from synthase was used in the isolation of emesoryed sequences from synthase was used in the isolation of emesoryed sequences from and two zucchini (CP-ACC 1A, LE-ACC 1B), LE-ACC 1B, ACC Synthases.

The remato (LE-ACC 1A, LE-ACC 1B) ACC synthases.

The run and two zucchini (CP-ACC 1A, and CP-ACC 1B) ACC synthases.

Contained in a plant host cell, generates RNA (hat is sufficiently complementary to an RNA transcript of an endoachous APT synthases.

Complementary to an RNA transcript of an endoachous APT synthases.

The reverse transcript of the antisense RNA (i.e. dNA) operably included to control sequences that effect its transcription into the ACC synthase gene by primer pairs encoding conserved APT synthases sequences. The DNA molecule can be used to delay ripening of temata or anceding femile.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Siles
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1.4%; Score 20, Ed. C.,
Best Losal Similarity 100.0%; Pred. No. 3.50e-04;
Matches 25, Conservative 0; Mismatches 0; indexis 0;
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Ionally FJ, Rine J, Stillman BW;
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514..1950
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16-DEC-1994, U14563.
16-DEC-1993, US-168479.
(COLD-) COLD SPRING HARBOR LAB.
(REGC.) UNIV CALIFORNIA.
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Li JJ, Mcnally FJ, Rine J,
WPI; 95-231507/30.
                                   02-APR-1992; US-86243.
10-SEP-1990; US-579896.
25-JAN-1995; US-378313.
07-JUN-1995; US-481171.
(USDA ) US SEC OF AGRIC.
Sato T, Theologis A;
WPI; 98-266005/18.
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    U7-JUN-1995; 481171
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Human trophinh cowa.
Trophinh. Lieffleton-seeleting protein. Lasting bysting lasting
Embryo implantation. Infortility, obli adhosion, therapy, diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant production of PIGII allows the study of the structure, function and role in non-generic of the protein. PIGII and truction acid encoding it can also be used to develop products for use in treating tumousts and canner and in the diagnosis of canner sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p-PSDB: R89895].
Now Isolated numbers acid encoding p53 response protein PIGI-1 reset to develop prods. for the study, diagnosis and treatment of theories and cancer. Staim 3: Pigure 5, 58pp, English.
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1.19. Solid 25. DB 17. Ledgth 1000;
Best Local Similarity 100 09; Prod 40; 7 (199104)
Habber 100; Consolitive 1. Mighthes 6, 113019 0.
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1.4%: Sorre DE: De 15: Length 2206:
Best Local Similarity 100:0%: Fred. No. 3.508-04.
Marches DE: Conserrating O: Mismatches O: Indels D.
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10-70-1999; UR8597.
12-71-1999; US-274318.
18-71-1999; US-274318.
18-00-1990: SRISTOL MYERS SQUIRE CO.
PHONE COMP. N. SPININGEL BR. Talboll R.
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[5-Apg-1996 (first entry)
p5% response protein PIGI-1 coding sequence.
"...esponse protein, PIGI 1, onscaponesis, dance.
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Homo sapiess.
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Mammalian trophinin and trophinin-assisting protein - used in infibiting or enhancing embry implantation, diadrosis of infertillity and treatment of cancer claim 16. Fig 3, 106pp. English.

A GENA -lone (118673) codes for human trophinin (#34889), a protein the cell mambrate of trophinist and uterine epithelial cells. It was obtd. from a trophoblast HT-H cell cDNA library Expressed in GCS-I cells using a cell allestic streenies protocol. The cDNA can be used for produ. of recombinant trophinin or its active fragments (see I18674-75), as a prote to fitted the presence of trophinin-encoding sequences, or can be introduced into cells to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           imprové trophini-mediated cell adhesion, e g. h. minimise emergo
implantation failure.
Sequence 2524 BP; 509 A, 648 C, 718 S, 654 T:
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This sequence encodes human epidermal transglutaminase. Primers 19911112 were used in the isolation of its cons.
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1.4%: Score 25: DR 19: Length 2524:
Bost Local Similarity 100.0%; Pred. No. 3.50e-04;
Matches 25; Conservative 0; Mismatches 0; Indeis 1
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28-MAR-1991: 05034.
28-MAR-1991: DP-065034.
(Abdes) Abcabanstrosokin res kenkvushu kk.
Well: 93:120381/15.
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04-0CI-1994; US-31752.
12-MAX-1995; US-430818.
(1591-) LA JALLA CANCEP PES FOUND.
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QDS711 standard, cDNA; 2781 BF.
Q25712;
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/*tag= a
2474..2479
/*tag= b
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/*tag= a
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                                                             W09610414-A1.
                     Polya_signal
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                                                                                   11-APR-1996.
                                                                                                                                                                                      Fukuda MN;
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States of Fig. 28, 75pp; English.

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1.48: Score 25: UB 4: Length 278:;
cul Similarity 100.0%: Pred. No. 3.50e.04;
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28-0820-1902 (first entry)
Sopouco el Drosophila heat short (actor (HSE) cDNA.
                                                                                    but shock tactor; stress condition; assay; ss.
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/**aa a
2723...2728
/*taa b
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26 - N -V - [1990] 48 - 6 [7991].

(TSSH.) NAT. [NST. OF HEALTH.

WHO. A. (TOS. J. WOSEWOOD JT.).
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/*tau- a
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D6-N V-1990; US-617910;
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Control Machania.
Control Machania.
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1-1-81841 RT3502,
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                                                                                                                                                                                                                                                                                          indistriction.
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and transformed yeat cells able to ferment lacture in when Disclosure: Fig 2: 35pp; English.

Claimed sequence includes a Beta-galactosidase lach acree from Aspergillus niger and the Abril yeast premoter in plasmid serior pVKI. The plasmid is used to transform a yeast expression system to produce BG extracellularly or into the periplasmic space, useful in fermenting lactose to produce Edge extracellularly or into the periplasmic space, useful in Sequence 3192 BP: 773 A: R74 C; 786 G; 759 T;
                                 The sequence encodes Drosophila heat shock factor protein and was obtained by screening a Drosophila heat shock factor protein and was obtained by screening a Drosophila genomic library with olinor nuclearlide protes (01237, 01328) based on the HSF anchor and sequence. The HSF sequence can be used to identify the HSF across to other organisms and also for the detection of stress or a discussed state in living systems. The gene can be used to increase expression of other genes. The gene can be used to increase together with other genes linked to host shock elements. It can be linked to a tissue-general or tissue-specific promoter and introduced into transgenic mice as a tool for cliniting increased or chronic stress response conditions as a model for how issues
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00.0%; Pred, No. 3.50e-04;
ative 0; Mismatches 0; Indels 0; Gais
                                                                                                                                                                                                                                                                               respond to chronic stress conditions such as those caused by viral
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Gene encoding major surface qp of rat P. carini.
Major surface glycoprotein; qpl16; rat; Pheumocysis varinis;
Vaccine: HTV; human immunodeficiency virus; diadnostic; PYP; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA construct contg beta-galactosidase gene and yeast promeder
                                                                                                                                                                                                                                                                                                 infection, chemical or mechanical stress. See also Uli2444 and
                                                                                                                                                                                                                                                                                                                                              631 C: 690 G: 629 1;
                                                                                                                                                                                                                                                                                                                                                                                          Length 2781;
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                                                                                                                                                                                                                                                                                                                                                                                   / Match 1.4%; Score 25; UB 2; UC Local Similarity 100.0%; Pred, No. 3.50e-04;
                                                                                                                                                                                                                                                                                                                                                                                                                              O. Mismatches
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5'sequence of yeast plasmid pVKll.
Beta-galactosidase, lacA+; pVKll; ds.
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Hartley BS, Ramakrishnan S, Kumar V;
WPI: 90-305026/40.
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in living systems.
Disclosure, Fig 2, 68pp, English.
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13-MAR-1989; GB-005674.
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Major Sections (1977)

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Will S2 154487/19.
Will S2 154487/19.
Will S4 154487/19.
Will S5 15
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Bost Local Similarity 100.0%; Pred No 3.50e-04;
Matches 25: Consertative 0: Mismatches 0: Indels
146.3412
1.1722
7.**ag= b
7.**ag= b
5.0.1. "Floyering Drivention By FOR"
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7.**ag= 0
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clones reactive with polyclonal serum were evaluated to identify those encoding 4p116. Three such clones (PCS. PCS and Pc14) were sequenced and contained ORFS encoding closely related but distinct profess. Although none of the clones contained the complete closes and generation of a putative composite sequence encoding a protein of ca. 122 kD. PCF was used to screen a second CDNA library constructed in modified lamplatable. Any VIELL Fig. 10 to contain ORFS encoding proteins similar to the original applic clones. GPB, GPP2, GF46 and GP14 were sequenced and were found to contain ORFS encoding proteins similar to the original applic clones. The TNA resistant of the protein should lead to understanding its role in the pathoenesis of P. carini, pre-encoding and may lead to understanding its role in the pathoenesis of P. carini, pre-encoding and may lead to understanding its role in the contain or pre-ention of information. The TNA relative may be used to make PCR primers for diagnostic use.

The true approach of the protein should lead to understanding its role in the contain or pre-ention of informations. The TNA relative may be used to make PCR primers for diagnostic use.

The true approach of the protein should be added to the contain the sequence below.

The true approach of the protein should lead to understanding its role in the sequence as a second diagnostic use.

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Pelease 3 1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

- n.a. database search, using Smith-Waterman algorithm

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MPsrch_en

Thu Jan 14 23:13:22 1999; MasPar time 2892.49 Seconds 1363.044 Million cell updates/sec Run on:

sof geserated Tabular output 2012-08-9⁶5-841-1 (1-1789) from (1809955841,seq 1789 Title:

Description:
Perfect Score:
N.A. Sequence:

. AAAAAAAAAAAAAAAAA 1789 1 GAATICAICIGICGACIGCI CITAAGIAGACAGCIGACGA

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 STD : Nmatch 567134 seqs, 1101898692 bases x 2

Searched:

Minimum Match 0% Post-processing:

Listing first 45 summaries

Database:

l:em_ba_2'em_fun_3'em_htg_4'em_hum1_5'em_hum2_6'em_in_7'em_cm_R em_or_9'em_ov_10'em_pat_11'em_ph_12'em_pl_13'em_ro_14'em_vi_enbank107

Database:

15.9b_bal 16.3b_bal 17 gt_htg 18 gt_in 19.9b_om 20.gb_ov 21.4t_pat 20.4t_bh 23.9b_stl 24.9b_ptl 25.9b_ptl 26.3t_ct_2 7 3t_ptl 28.9b_stl 24.9b_ptl 25.3b_ptl 30.3t_ct_n 7 3t_ptl 28.9b_stl 26.9b_stl 31.9b_sy 30.3t_n 7 3t_ntl

Variance 8 232, scale 1 435 Mean 11.810. Statistics: Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description	Pred. No
	1787	0.00	1789	2.6	HST40282	Homo sapiens integrin-	0.000+0
C1	1336	74.7		28	MMU94479	Mus musculus integrin	0.00e+0
ر. د ا	001	11.1	C1 C1	٠ <u>.</u>	319940	human STS A002C40, seq	9.79e-9
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ALIGNMENTS

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RESULT 1 LOCUS DEFINITION ACCESSION NID KEYWOPDS	SOURCE ORGANISM	FEFERENCE ATHORS	TITIE	MEDLINE REFERENCE AUTHORS TITLE	JOURNAL	REFERENCE AUTHORS TITLE JOURNAL	PEMAPK COMMENT FEATURES SOUTOR

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VKVLKVRDWSTRKSPDFNEECPPLPIFSHPNVLPVLSACQSPPAPHPTLITHWMPYGS
LYNVLHEGTNFVVDQSQAVKFALDMARGMAFLHTLEPLIPRHALNSRSVMIDEDMTAR
ISMADVKFSFOCPGRMYAPAWVAPEALQKKPEDTNRRSADMWSFAVLLWELVTREVPF
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/coll_line="HeLa"
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/translation="mddlftqcreganvavrlmldntendlngdddhgfsplhwacre
gpsavvemlinggar navmregddtplhlaashghrdtygklloykadtnavrehgnv
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ADLSNMFIGMKVALEGIRPTVPPGISPHVCKLMKICMNEEDPAKRPKFDMIVPILEKMO
                                                                                                                                                                                                                              Li.F., Liu.J., Mayne,R. and Wu.C. Identification and characterization of a mouse protein kinase that is highly homologous to human integrin linked kinase Blockhim. Blockhim. Blockhim. Blockhim. Blockhim.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (18-MAR-1997) Cell Biology, University of Alabama at Birmingham, 1670 University Blvd., 217 Volker Hall, Birmingham, AL 35294-0019, USA
                      Mus musculus integrin binding protein kinase mRNA, complete cds. U94479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 TCAATCAGGGGGATGATCATGSCTTCTCCCCTTGCACTGGGCCTGCCGAGAGGCCGCT 252
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/strain="BALB/c"
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/chromosome="7"
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                                                                                                                                                                                                                    613 CATICIGGAAGGGAGCACICGCACAAGGCGCGGAAAIGGGAACHTAAAAAAAAAAATAGG 672
                                                                                                                                                                                                                                                                                             673 GTATTGACTTCAAACAGCTCAACTTTCTGGCAAAGCICAATGASAATGATTGTGGAGAGG 732
433 CATGITICIGGGGCGAAGACCAGGIGGCAGGAAGAAGTGGIGGCIAACGGGGGIGIIGIGA 492
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                   596 TICTCCGAGAGCGGCAGAGAAGATGGGCCAGAATGTCAAAGGATATGGATATAAAAGAACA
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/note-"TBP-associated factor II 30"
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Pred No. 9 79e-93;
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/db_xref="taxon.9606"
/chromosome="11"
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/haplotype="23"
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             1533 CCAAAAANNAANTGAGACTTAGATTTGTCACTTGGGAGATGATGTGTGGGAACATGGGAG 1692
                                                                                                                                   1572 AFCALGGIAGIACIACCCASITALGGGACITGITCCCTGCCAGCCAGCCIACCACGGTAGCC 1632
                                                                                                                                                                          24-JUL-1996
                                                                                                                                                                                                                                                                                                                                                            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 222)
                         Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                           SIS: SIS sequence; primer; sequence tagged site
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ., Rockville, MD 20859
                                                                                                                                                                                                                                                      G19940 222 bp DNA human STS A002C40, sequence tagged site.
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Primer B: CCTATCCTTGAGAAGATG
STS size: 222
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Total Volume:
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/db_xref="FID.g2193966"
/translation="MSCSGSGADPEAAVASAASAIGPAPPVSAVAAIGSSTAAENKAS
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ANGDVKPVVSSTPLVDFLMQLEDYTPTTPDAVTGYYLNRAGEEASIOPTTPLTSTAAG
KFISDIANDALGHCKMKGTASGSSPSKSKDKKYTLIMEDLTFALSEYGTNVKKFHTFT
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Submitted (27-APR-1995) Laszle Tora, CNPS Pesorm UFP, Inet, de
Genetique et de Biologie Moleculaire et Cellulaire, Illkirch CEDEX,
                                                                                                                                                                                                                                                                                                                                                                                                                         HSU25816 2605 bp DNA PRI 16-JUN-1997
Human TATA-binding protein associated factor II-30 (TAPLES) denover
complete cds.
U25816
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/product="TATA-binding protein assa late: fort.r 20 kDa
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Vertebrata; Mammalia; Eutheria, Primatos; Catarrhini; Hominidae;
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Organization and chromosomal localization of the grue (TAFZH)
encoding the human TRP-associated factor II 30 (TAFIL10)
Genomics 29 (1), 269-272 (1995)
96079120
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2263. 2352)
/gene="TAFII30"
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Score 177; DB 26; Length 2605;
Pred No 7 76e-80;
0; Mismatches 2; Indels 3; Gaps
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Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
Pecombinant fowlftex virus
Patent: uS 5670367-A 14 23 SEP-1997;
Location/Qualifiers
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                  Pred No 7 76e-1
0; Mismatches
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Sequence 14 from patent US 5670367.
155494
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| 1491 c 1486 g
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Local Similarity 97 5%;
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DEFINITION Homo sapiens chromosome 5, BAC clone 11933 (LBNL H175), complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1108 CATGCACTCAATAGCCGTAGTGTAATGATGAGAAAAGACTGCCGGAATTAGCATG 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  988 TACAATGTACTACATGAAGGCACCAATTTCGTGGTGGACGAGGCAAGCTGTGTGAAGTTT 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1048 GCTTTSGACATGGCAAGGGGGAIGGGCTTCCIACACACIAAAAGCGCICAIGGGAGGA 1107
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Kimmerly W., Bondoc, M., Cheng, J., Connolly F.S., Gunning, K.M., Radner, K., Miguel, T., Miller, C., Pitlyck, S., Pollard, M., Pojeski, H., Subramanian, S. and Martin, C.H., Sequencing of human chromosome 5
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Primates; Catarrhini; Hominidae; Homo.
                  23-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 7218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.85e-07;
206; Mismatches 153; Indels
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Dorner,F., Schelflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
                        PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.6%, Score 46, DB 21; Best Local Similarity 0.8%; Pred. No. 1.86e-07; Matches 3; Conservative 206; Mismatches 163
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| 1491 c 1486 g 1929 t
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ACCESSION 166494
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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US-08-955-841-1.rge

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Larue Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System
                                           A (bases 1 to 74371)
Kimmerly,W , Rondorc,M , Cheng,T., Connolly,K S , Gunning,K M.,
Davis,G A , Kadner,K , Miguel,T , Pitiuck,S., Pollard,M.,
enjeski,H., Subramanian,S. and Martin,C.H.
                                                                                                          Direct Submission
Submitted (01-AUG-1998) Human Genome Center, DOE Joint Genome
Institute, Lawrence Berkeley National Laboratory, MS 74-157,
Berkeley, CA 94720, U.S.A.
Sequence submitted by:
DOE Joint Genome Institute.
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                                                                                                           TITLE
JOURNAL
                               JOURNAL
                                                REFERENCE
                                                               AUTHORS
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 TITLE
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/noter"SFALL 0 expellent exent trame 0"
28987 24214
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19305. .1958*
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complement(16993, .17085)
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Large Scale Sequence Analysis and Annotation with the Sequence
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Davis,C.A., Kadner,K., Miguel,T., Pitluck,S., Pollard,M.,
Rojeski,H., Subramanian,S. and Martin,C.H.
                                                                                                                                                                                                                                                                            Submitted (01-A0G-1998) Human Genome Center, DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, MS 74-157, Berkeley, CA 94720, U.S.A.
Sequence submitted by:
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /standard_name="RLF"
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      Kadner,K., Miguel,T., Miller,C., Pitluck,S., Pollard,M.,
Rojeski,H., Subramanian,S. and Martin,C.H.
Sequencing of human chromosome 5
Unpublished
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9070. .9387
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12057. 17007
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6647. 6601
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/note="(CA)19"
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12365. .12645
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Complement(37595...37654)

Complement(join(38063...38218,38462...38578,38741...38995,3971...38205,39532...40661,41868...41972,42103...4225,42492...42569,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 15923 STSKCSCMSPSKSKPGWGYPSWKKYPCAMWMTCKSSKCWCWSYRMRMKCYSCSYCYCSSG 15982
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/note="78%-100% protein identity GenPept:U18937"
complement(38069: 38215)
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                                     /note="GRAIL 2 excellent exon, frame 1"
complement(32.59. .32.32)
/note="GRAIL 2 excellent exon, frame 2"
32.388. .32488
                                                                                                                                                                                                                                                                        /note="GRAIL 2 excellent exon, frame 2" complement(35238. .35331)
/note="GRAIL 2 excellent exon, frame 1" 36392. .36663
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3501. .3722
/nose1. .3722
/db_xref="abeST:AI025011"
36901. .37164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /standard_name="STSG-9983"
/db_xref="dbSTS:G26554"
/rpt_family="MIR" complement(31573. .31724)
                                                                                                                                                                                                              complement(33570. 33785)
/rpt_family="Alu"
                                                                                                                                                                                                                                                     .34144)
                                                                                                           /rpt_family="MLT1"
32617. .32908
                                                                                                                                                                                           /rpt_family="MLT1"
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32977. .330AA
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/rpt_family="MER20"
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/note="GRALL 2 excellent exon, frame 0"
28987. .29214
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complement(22538. .22981)
/standard_name="possible repeat"
23022. .23326
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15300. .15613
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complement(17678 1827C'
/rpt famil
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complement(16675, .16977)
/rpt_family="Alu"
complement(16993, .17085)
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27191. 27477
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complement(14906.
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16571, 16690
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21736. .22035
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23473. .23761
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23744. .22767
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14175. .14470
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13783. .14024
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28712. .2893
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complement(35238. 35331)
/note="GRAIL 2 excellent exon, frame 1"
/note="GRAIL 2 excellent exon, frame 1"
/note="GRAIL 2 excellent exon, frame 1"
                                /standard_name="A1027942"
/note="note indentity Fer roysdaln x1"
complement(30401. 30536)
/note="GRAIL 2 excellent exon, frame 2"
complement(20692. 30733)
/rpt_family="MIR"
complement(31573. 31724)
                                                                                                                                                                                                                                                                                                                                                                                                /note="GPAIL 2 excellent exon, frame 1" complement(32159, 32222) /note="GRAIL 2 excellent exon, frame 2"
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complement(33670, .33785)
/rpt_family="Alu"
complement(34021, .3414)
/note="GRAIL 2 excellent ex
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/db_xref="dbSTS:G26554"
complement(37595, 37554)
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32977. .33088
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Query Match
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/db_xref="PID:g464028"

/db_xref="PID:g464028"

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VRQEARLFAMLAHPNITALKAVCLEEPNICLVMEYAAGGPLSRALAGFRVPPHVLVNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVQIARGMHYLHCEALVPVIHRDLKSNNILLLQPIESDDMEHKTLKITDFGLAREWHK
TIQMSAAGTYAWMAPEVIKASTFSKGSDVWSFGVLLWELLIGEVPYRGIDCLAVAYGV
AVNKLTLPIPSTCPEPFAQLMADCWAQDPHRRPDFASILQQLEALEAQVLREMPRDSF
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EVFERELTILLIOOVDPERPHVRRRGTFKRSKLRAPDGGERISMPLDFKHRITVVASP
GLDRRRNVFEVGRGDSPTFPRFRAIGLEPAEPGGAWGRQSPPPLEDSSNGERPACWAW
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PAPPARAGSSGIPKLIGPAKLIGPALASAGJAPDLGPSPOSPERGSSPTTPPTPT
PAPCPIEPPSPSPLICFSLKTPDSPPTPAPLLLDLGIPVGGRAKSPREEEPRGTV
PPPGITSRSAPGTPGTPRSPPLGISPPPSPLRSPIDPWSFVSAGPRPSPLSSPLPSPQPAP
                                                                                                                                                                                                                                                                 domain-containing proline-rich kinase with serine/threonine kinase
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                                                                                                                                Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="submitter comments: serine/threonine protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kinase, proline-rich, src-homology 3 (SH3) domain,
leucine/isoleucine zipper motifs"
                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (15-MAR-1994) Paul J. Godowski, Genentech, Inc.,
Point San Bruno Blvd., South San Francisco, CA 94080, USA
Location/Qualifiers
1. 3531
                                                                                                                                                                      1 (bases 1 to 3531)
Gallo,K A., Mark.M.R., Scadden,D T., Wang,Z., Gu,Q. and
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Pred. No. 1.88e-02;
0; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                         Chem. 259, 15092-15100 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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1207 c 1143 g
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1710. .1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="gt_10"
/cell_line="CMK11-5"
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/note="SH3 domain"
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Godowski, P.J.
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Best Local Similarity ·83.0%;
Matches 44; Conservative
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Submitted (15-MAR-
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complete cds.
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/note="amino acid feature: SH3 domain, bp 613 . 789;
amino acid feature: leuchne zipper basic region, bp 1686
1932; amino acid feature: Friling-rill region, pp 2465
. 2839
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/db_xrcf="PID:9488296"
/translation="MEPLKSLFLKSPL5SWNGSGSGGGGGGGGFFEGSPKAAGYANP
                                                                                                                                                                                                                                                  Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata; Vertebrata; Eutheria, Frimates, Catainhini, Hominidae: Humo. 1 (bases I to 358)
Ing.Y.L., Leung.I.W., Heng.H.H., Tsui.L.C. and Lassam,N.J. MLK-3: identification of a widely expressed protein kinase hearing an SH3 domain and a leucine zipper-basic region domain oncogene 9 (6), 1745-1750 (1994)
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                                                                                                                                                                                                  MLK-3 gene; protein kinase.
Homo sapiens (tissue library: lambda gilf) thymus cDNA is mPNA.
Homo sapiens
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1211 c 1161 q 551 t
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1276 GACATGIGGASILIIGCAGIGCIICIGIGGGAACIGGIGACACGGGAGGIACC 1328
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Local Similarity 83.0%; Pred. No. 1.88e-02;
les 44; Conservative 0; Mismatches 9;
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/tissue_lib="lambda gtl0"
/map="11 g13.1-13.3"
482. 3025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"/db_xref="taxon:9606"
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482. .3025
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DEFINITION Sequence 21 from patent US 5635177.
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Submitted (24-JUL-1998) The Institute for Genomic Pesearch, 9712
Medical Center Dr. Pockville, MD 20850, USA
Medical Center Dr. Pockville, MD 20850, USA
Address all correspondence to: Mark Adams The Institute for Genomic Pesearch 9712 Medical Center Dr. Pockville, MD 20850, USA e-mail address: humgenétigr.org. The orientation of the sequence is from SPE end to 77 end Genes were identified by a combination of five methods including: XGRAIL (available by anonymous ftp from arthur.epm.cnl.gov), Genéfinder (Phil Green, University of Mashington), Genscan (Chris Burge, http://gnomic.stanford.Edu/-chris/GENSCANW html)searches of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complete sequence against a peptide database, and the Human generate Adabase at TIGR (http://www.tigr.org/tdb/hgi/hgi/hml).
Genes without peptide homolgy having spliced ESI hits are termed 'Unknown gene product'. Genes encoding tRNAs are predicted by tPNAscan-SF (Sean Eddy, http://genome wistl edu/eddy/tRNAscan-SE/).

Location/Qualifiers

1. 216021
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//dr.xref="taxon.9606"
//chromosome="15"
/map="#16G21-22"
/mosp="#495EF10"
27765. 27872
/note="7766, STS1-cSPL-27g3-uA/cSPL-27g3-uZ, Chr. -, Homo
                                                                                                                                                                                                                                                                              Submitted (02-JUN-1998) The Institute for Genomic Research, 9712 Medical Center Dr. Reckville, MD 20850, USA, Email:
                                                                                          1 (bases 1 to 21601).
Adams, M.D., Loftus, B.J., Zhou, L., Crosby, M., Fuhrmann, J., Masun, T.M., Rrandun, F., Kim, G.J., Kerlavage, A.F. and Venter, J.C. or sapiens Chromosome 16 BAC clone CIT9875K-A-952F10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146. KSMPPAPRPSSAGKKKKKYYYYYGYYYYYYYYYPOMSRAMMAAAWYYKPRSCMAWYYYMPGF 1521
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                                                              Eukaryota, Metazoa, Chordata, Vertebrata, Mammalia, Eutheria,
Primates; Catarrhini; Hominidae; Homo.
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/note="7408, STS1-cSPL-24g1-3A/cSPL-24g1-02, Chr
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/db_yref-"dbsTS-G04338"
| 51778 G 49172 g 53987 t 124 others
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/db_xref="dbSTS:G09935"
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./notea="16084, GHL; 3cT10B02,
./db_xref="dbSTS:G09703"
175810 175945
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Adams, M.D. and Loftus, B.J.
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Adams, M D and Leftus, B J.
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/translation="papertpolitypervam" il nypaeletterpy the pptttninggr
isodetepmybeappparppykyydptrabroch ttyvymmyd (himpyladylesde
kekiptavkpalemidlingsaekppyppyi ppyfavtnpttiavygksglassgsss
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The tobacco luminal binding protein is encoded by a multigrne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NTBLP3 800 bp RNA PLN 03-DEC-1993 Nicotiana tabacum blp3 mKNA for luminal binding protein (BiP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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Sabelited (12-IUN-1941) [ Portermor Plane Temotic Systems.
Plateaustraat 22, R-9000 Gent, REIGIUM
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Magnollopsida; Solahanac: Solanales; Solanaceae; Nicotlana.
1 (bases 1 to 800)
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Bukaryotae; mitochondrial eukaryotes; Viridiplantae;
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/prodoct="luminal birding protein (Bir)"
77.
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Bennett, B.D., Gueddel, D. and Matthews, W.
Protein tyrosine kinase agonist antibodics
Patent: HG 5635177-A 21 03-30N-1997.
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Job time : 2919 secs
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/db_wrof."Prin a2318115"
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/translathplwvltAAHCKKWVLSLIAAAWAEEQNKLVHGGPCDKTSHPYQAALYTSGH
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HDQDIMLLRLARPAKLSELIQPLPERDCSANTTSCHILGWGKTADGDFPDTIQCAYI
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GSKEKPGVYINVCRYINWIQKTIQAK"
- 434 c 367 g 308 t
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Stephenson, D. and Clemens, J.
Zyme CDNA isolated from AD brain tissue
2. The CDNA isolated from AD brain tissue
3. (bases 1 to 1451)
1. Ittle, S. P. Johnstone, E. M. and Norris, F.
Direct, Submission
Submitted (15-301-1997) CNS bivision, Eii Lilly and Company, Lilly Corporate Center, Indianapolis, IN 45285, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Zyme; protease bears homology to Kallikrein class and can be localized to microvessels and microglia; chymotrypsin-like"
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Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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Homo sapiens MutS homolog 5 (MSH5) mPNA, complete cds.
AΕΌ48986
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/db_xref="taxon.9505"
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Her,C. and Doggett,N.

Direct Submission

Submitted (17-FEB-1998) Life Sciences Livision and Center for Human Senome Studies, Mail Stop M888, Los Alamos National Laboratory, Los Alamos, NM 87545, USA
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/db_xref="PID:g3108220"
/translation="MASLGANPPFTP@SPFGAASSGFFSPAPVFGFREAEEEEVEEE
Eukaryote: Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Frimates. Catarhin; Hominidae, Homo 1 (bases 1 to 2872)
Her, C and Doggett,N A Cloning, structural characterization, and chromosomal localization of the human orthologue of Saccharomyces cerevisiae MSH5 gene Genomics 52 (1), 50-61 (1998)
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Best Local Similarity 94.7%; Pred. No. 5.03e-02;
Matches 36, Conservative 9; Mismatches 2;
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Pelease 3 lA John F. Collins, Biocomputing Pesearch Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

- n a database search, using Smith-Waterman algorithm

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>US-08-955-841-1 (1-1789) from MS08955841.seq 1789 Description: Perfect Score: N A Sequence:

AAAAAAAAAAAAAAAAA 1789 TTTTTTTTTTTTTTTTT 1 GAATTCATCTGGGCTGCT CITAAGTAGAGAGTGAGGA

TABLE default Gap 6 Scoring table:

188442 seqs, 68026449 bases x 2 Searched.

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Nmatch

Minimum Match 0% Post-processing:

Listing first 45 summaries

Database:

n-geneseq32 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part19 10.part10 11.part11 12.part12 13:part13 14.part14 15.part15 16:part16 17.part17 18:part18 19.part19 20:part20 21.part21 22.part27 28:part28 24.part24 25:part25 26:part26 27.part27 28:part28 29:part24 30:part36 31:part31 32:part32 33:part33 34:part39 40:part40

Mean 9.634; Variance 6 948; scale 1.386

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	Ú,00e+00	5.09e-10	4.81e-09	1.18e-06	3.49e-06	1.02e-05	8.51e-05	2.43e-04	6.85e-04	6.85e-04	6.85e-04	6.85e-04	6.85e-04
Description	Human integrin-linked	Base substituted E.co	Oligonucleotide probe	Cligonucleotide probe	Base substituted E.co	Generic DNA sequence	PTK gene LpTK4 partia						
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ALIGNMENTS

New isolated integrin-linked serine/threonine kinase - used to develop products to modulate oul growth, adhesion, migration and invasion, e.g. for treating cancer or inflammation

Invasion, e.g. for treating cancer or inflammation

Sclaim 3: Fig las Gipp: English.

Colaim 3: Fi 19-SEP-1997 (first entry)

Human integrin-linked kinase (ILK) cDNA.

Integrin-linked kinase, ILK; serine/threcoine kinase; cell growth; cell adhesion; cell migration; cell invasion, inhibitor; gene therapy, diagnostis; carcer; leuka-mia, t.m..r, inflammation; arthritis; osteporosis; cardiovascular disease; ss.

Homo sapiens. Location/Qualifiers T 1 T71716 standard; cDNA; 1786 BP. 157..1512 /*tag= a 1749 1754 /*tag= b 03-JUL-1997. 19-NGV-1996; CA0760. 21-DEC-1995; US-009074 (DEDH.) DEDHAR S. (HANN.) HANNIGAN G. Dedhar S. Hannigan G; WPI; 97-351062/32. WPI; 97-351062, P-PSDB; W18211 WO9723625-A1. polya_signal

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acids (including antisense) can be used in gene therapy to inhibit the expression for the treatment of e.g. cancer, leakaemia, solid tumcurs, chronic inflammatory disease, arthritis, esteoporosis and candicoascular disease, and can also be used as diagnostics to
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egeatgtatgeaeelgeetgggtageneergaanetetgnagaagaunetgaadund
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                                                                                                                              1091 cacacactagageeeefinatiiinacdacatqeactcaataqeedtaqtaqtaqtaatfdd;
                                                                                                                                                                              gaggadatgadtgoddgattagdatgadtgtdaagttetetettt.cdaatgteetqat
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E.coli beta galaciusidase alphanfraumout, baso substitutious:
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187..204
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N81164;
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                                                                                                                                                                            nisincorporation, completion of molecules and screening.

Disclosure, p. English.

English were introduced into the alpha fragment of Endom point mutations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified at all to variable 3 ends generated in this way are used as primers for variable 3 ends generated in this way are used as primers for the reperse transcriptase. Nucleotides are misincorporated by the amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which cocurred singularly in any given mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 tthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynvhnhn 149
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                                                                                                                                        Introducing random point mutations into nucleic acods -
by prepn of single stranded template, annealing a primer, elongation,
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                                                                                 Nonett of:
Knowles J, Koivula A, Bamford J, Reinikainen T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide probe MK14-A
Oligonucleotide: DNA probe: mycobacteria; disease diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47; DB 1; Length 204;
Fred. No. 5.09e:10,
50: Mismatches 28; Indels
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26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
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                                                                      (SUSO) SUOMEN SOKERI OY.
                                                03-APR-1987; US-034819
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WPI; 93-378844/48.
05-MAY-1988.
30-MAR-1988; 105163.
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                                                                                                Lehtovaara F, Know
WPI: 88-279927/40.
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01-DEC-1993.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions: ss.
Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide probe MX14.7A consists of nucleotides 5.95 of (u51735). It hybridized to all spp. of myochacteria tested cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection see also 051735-45 and 051747-59.
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                                                    31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe, mycobacteria, disease diagnosis;
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by prepn of single stranded template, annealing a primer,
misincorporation, completion of molecules and screening.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.2%, Score 40, DB 9, IV
5.8%; Pred. No. 1 18e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     occurred singularly in any given mutant. See also P80575. Sequence 204 BP; 21 A; 47 C; 17 G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 14; 23pp; English.
Q51746 standard; cDNA; 91 BP.
                                                                                                                                                                                                                                                                                                   (BECT ) BECTON DICKINSON CO.
Shank DD, Spears PA;
WPI; 93-378844/48.
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N81164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-034819.
                                                                                                                                                                                       EP-571911-A.
01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651
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30-MAR-1988; 105163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Rest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 BP;
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                                                                                                                                                                Synthetic.
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Disclosure; Parenting comman and an effector gonath property appropriate property of the prope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receiver some degree of conformational rigidity to the peptides. The TSAKs of company comprising a TSAR binding domain can be used in vivo to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      that the expressed peptide mentains 2 or 4 systeine residers positioned in, or flanking, the unpredicted or variant residues. These residues
                                                                                                                                                                       91 thhyrrmrbnyrd-ynrsdaaawyccyrrsykydccynachbddhywyb-bbwynyhnh 148
                                                                                                                                                                                                                                                                          408 TOGDAGIGSTAGGIGSOLGSONAGIOPONAGSIGSTIONIGALGGIAGIGIGALGAIGAGAGI 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Generic DNA sequence to generate a random TSAR petide library. TSAR, totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid, detection, screening, treatment, generic, ss.
                                                               Sabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain
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/note~ "this sequence represents '2'; 2 can be a
sequence of 6, 9 or 12 nucleotides (see
commonts)"
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larity 5.48: Prod. No. 1.02e-05;
Conservative 33; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                968 GGATGCCGTATGCGTCTACAATGTACTACATGAAGGCAGCAAT 1014
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                        149 nnenecebanhyehnyhbnahrawayvrhdarrddyheeveheegat 195
Pred. No. 3.49e-06;
57. Mismatches 34.
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070468 standard; DNA; 114 BP.
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Fowlkes DM, Kdy BK;
WPI; 94-2797 89/84.
Best Local Similarity 13.1%:
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other specific peptides generated by these generic sequences are shown in P6K191-54. TSAPs are concatenated beternfunctional proteins or peptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        that the expressed peptide contains 2 or 4 cystoine residues positioned in, or flanking, the apprehisted or variant residues. These residues confer some degree of conformational rigidity to the paptides. The TSARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       that are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying proteins or peetide(s) which bind a Bluand - by screening a recombinant vector library expression lusion proteins comprisating a binding domain and an effector domain.

Pisclosure, Page 35: 255pp. Endlish.

V70465 is a generic DNA sequence used to generate random TSAR (Totally Synthetr Affinity fempents) peptides. This deneric formila can also be represented as follows. X(NNH)6(TGC)(NNH)112(NNH)14(TGC)(NNH)3 Y and Y are fearly in restriction sites (X is not the came as Y) that are not securify and faither other generic sequences are shown in V70465-68.
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TSAR; totally synthetic affinity readent; synthetic; binding domain;
effector domain; concatemented heterotunctional professor linker;
direct; rapid; detection, screening, treatment; generic; ss.
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for complex methods of hybridoma formation or in vivo antibody
production. The ISAEs are easily characterised and have designed
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6.3 benabanbanbanbanben gennbanbanbanbanbanbanbanbanbanb 114
                                                                          349 GGITCALLACALLSAICCGIGCCCCCCCAIGAICAACAICTCAACTACACC 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/mole= This sequence represents (2) 2 a
sequence of 6, 9 or 12 nucleotides (see
comments)...
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                                                                                                                                                                                                                                       070465 standard; DNA; 114 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.08;
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US-08-955-841-1.rng

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Proceeding a binding of potential within bind a ligand - by comprising a binding domain and an effector domain a ligand - by defending a binding domain and an effector domain proteins bisolosure; page 55, 255pp; English.

Disolosure; page 55, 255pp; English.

CCC (NNB)62 (NNB)67 (NNB)67 (NNB)67 (NNB)10.

This generic formula can be represented as follows. X(TGC)(NNB)10.

(TGC)(NNB)62 (NNB)67 (NN
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             77-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR peptide library.
TSAR: totally synthetic affinity reagent: synthetic, binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct, rapid, detection, screening, treatment, generic, ss:
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                                                                                                                                                                                                                                                 //octs "this sequence represents 'Z'; Z can be a sequence of 6,9 or 12 nucleotides (see comments)"
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(2)
                                                                                                                                                                             Location/Qualifiers 55..60
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Sequence 114 BP; 0 A; 4 C;
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31-JAN-1994; US-189331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fowlkes DM, Kay BK; WPI: 94-279739734,
                                                                                                                                                                                                                                                                                                                                                             18-AUG-1994
01-FEB-1994; U00977.
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referring a recombinant vector library expressing fusion proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain bischosure; Page 35; 255pp; English and an effector domain bischosure; Page 35; 255pp; English and an effector and TSAP (Totally Synthetic Affility Posquence used this generate random TSAP (Totally Synthetic Affility Posquence used this generated as follows: X(NNB) LITGC)(NNB)66(NNB)7 (15C)(NNB)10Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generated by these generic sequences are shown in C70466-68.

Cother specific peptides generated by these generic sequences are shown in R65151-54. TSARs are concatenated helecofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active They may further comprise a linker period between the 2 domains the oligonucletides are also desirred so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             that the expressed populations is not described and also designed of in, or flanking, the unpredicted or variant residues. These residues on for some degree of conformational rigidity to the peptides. The ISARs or compens. Comprising a ISAR binding domain can be used in vivo to deliver a chemically or biologically active moicty, eq. metal ion, radioisotope, peptide, toxin or enzyme, it the specific inraging to the monoclonal or polyclonal artibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo unlibody production. The ISARs are easily characterised and have designed activity allowing direct and reapid detection in a screening process.
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(UXNC-) UNIV NORTH CAROLINA.
FOWLKS DM, KAV RK:
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Best Local Similarity
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W09418318-A.

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Scribbally proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins remember a recombinant vector library expressing fusion proteins of computational by 25 per per section of the protein proteins of the protein plant and an effector domain specification by 25 25 per per section 25 perides. This generic formula can also be represented as follows: X(NNB) EG(NS) 12 (NNB) EG(NS) 12 (NNB) EG(NS) 12 perides as follows: X(NNB) EG(NS) 12 (NNB) EG(NS) 12 (NNB) EG(NS) 12 (NNB) EG(NS) 13 per the same as Y) that are not specified further observed by those generic sequences are shown in period further concatenated between the sequences are shown in period further concatenated between the sequences are shown in period at least two functional regions - a binding domain with a fiftinty for a ligand and a second effector peptide portion that is committed by the superiod proteins or peptide sequences are also designed in a figure of contains 2 or 4 dysteine residues positioned in or finishing, the unpredicted or variant residues positioned in or compens. Generally or binding domain can be used in vivo to deliver a chemically or binding domain can be used in vivo to deliver a chemically or binding domain can be used in vivo to deliver a chemically or binding domain can be used in vivo to deliver a chemically or binding domain can be used in vivo to the components of the contains and cont
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                                                                                                                                                                                                                (UYNC-) UNIV NORTH CAROLINA.
Fowlkes DM, Kay BK;
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Identifying proteins or peptido(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins. Per screening a recombinant vector library expressing this on proteins. Per comprising a binding domain and an effector domain can also be disclosure; Page 35: 255pp; English: This general formula can also be synthetic Afficiaty Keaperils) peptides. This general formula can also be synthetic Afficiaty Keaperils. Peptides. This general communication because of any are flaming restriction sites (X is not the same as Y) that are constructed as follows: X(NNB) 6(70) (NNB) 2(NNB) 7(70) (NNB) 7(70) (NNB)
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970465 is a generic ENA sequence used to denotate random TSAM (Totall);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1159 IICGGGCAGICCAIGICCICAICAACAAIAACACIACGGGTATIGAGTGCATGTGGGA 1100
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TSAK: totally synthetic affinity redeemt, synthetic binding demain;
effector domain, concatencated beteroinerilonal projects. Hisker:
direct; rapid; detection; screening; treatment; evencie; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying proteins or peptide(s) which bind a linuad - by screening a recombinant vector library expressing fusion proteins complising a binding domain and an effector domain.
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comments)"
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01-FEB-1993;
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Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)6(TGC)(NNB)11Z(NNB)14(TGC)(NNB)3Y. X and y are flanking restriction sites X is not the same as Y) that are not specified further other generic sequences are shown in 70466-68 other specified further other generic sequences are shown in 70466-68 other specified peptides generated beterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with a figurative for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. They may further comprise a linker peptide between the 2 domains. They may further comprise a linker peptide between the 2 domains. They may further comprise a linker peptide between the 2 domains. They may further comprise a linker peptide between the 2 domains. They may further comprise a linker peptide between the 2 domains. They may further comprise a linker confer some degree of conformational rigidity to the peptides. There residues confer some degree of conformational rigidity to the peptides. The TSARs of a composing an also replace the function of macromolecules, egg.

Celliver a chemically or biologically active moiety, eg. metal ion, monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody activity allowing direct and antibodies and have designed activity allowing direct and rapid detection in a screening process squence 114 BF: 0 A; 2 C; 2 C;
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pIK gene LpIK4 partial seguence.
pIK; protein tyrosine kinase; catalytic domain; c-kit; megakaryocyte;
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The LPTKs are expressed in lymphocytic cells, as well as megakaryocytic cells. Sequencing of LPTK-4 revealed the sequences given in 049751 and 049751.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 114;
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32; Mismatches 75; Indels
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Claim 2; Fig 5; 60pp; English.
pTK genes were identified using two sets of degenerative
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040755 standard, DNA, 404 BP.
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Best Local Similarity 4.5%,
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14-NOV-1996 (first entry)
Growth regulatory protein cNNA, GRP-5', isolated using Hel-Nl.
Growth regulatory protein cNNA, GRP-5', isolated using Hel-Nl.
Human, neurou-specific protein, Hel-Nl, 3'-UTR instability sequence;
paraneoplastic sensory neuropathy; oncoprotein; lymphokine; rat: elav;
RNA recognition motif; RRM; Drosophia; cellular growth; localisation;
instability, translatability, neurons, autoimmune protein, FE. FCD: PSN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Against antibodies which activate specific protein tyrosine kinase(s) - also activate chimeric proteins of kinase extracellular domain and ye constant domain, useful for studying, and therapeutic modulation of cell growth and differentiation bisclosure; Page 58-59, 125pp; English.

DNA probes based on protein tyrosine-kinase (pfK) sequences were used partial sequence (T03099) was isolated from a lymphocytic cell library. The partial sequence can be used to identify other new pTK genes, or to design drugs, peptides or antisense constructs that modulate pTK activity, 95-A; 106 C, 123 G, 77 T;
                                                                                                              Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag* a
/noter "base n at position 212 is not identified
in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= b
/mote= "base n at position 222 is not identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note* "base n at position 321 is not identified in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1275 GASAIGIGGAGIIIIGGAGIGCIICIGIGGGAACT56T6AAAGGGAGGIACC 1328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
                                                                                                                                                    273 gacytotygagttttgggggtgctgctgtgggaactgctgaccggggagntgcc 325
is claimed (claim 7) and stated as given in the specification, however is missing from the publication. Sequence 404 BP; 95 A, 106 C, 123 G, 77 I;
                                                                                                                                                                                                                                                                                                    14-FEB-1996 (first entry)
Protein tyrosine-kinase LpTK4 DNA fragment.
Protein tyrosine-kinase, pIK; LpTK4, agonist: cell growth; differentiation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16; Length 404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0, Mismatches 10; Indels
                                                                             Length 404;
                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matthews W, Isai SP;
                                                                                                                  Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.85e-04;
                                                                                              5 85p-04;
                                                                       Query Match
1.9%; Score 34: DB 8:
Best Local Similarity 81.1%; Pred No. 6 95e-04
Matches 43; Conservative 0, Mismatches 1
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1 1%; Pred No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goeddel D, Lee JM,
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                                                                                                                                                                                                                                                                   ro3098 standard; DNA; 404 BP.
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Matches 43; Conservative
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(GETH ) GENENTECH INC.
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04-APR-1995; U04228.
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WPI; 95-366160/47.
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PUT Product of CDMA library for related proteins - by screening total cell
menn with RNA-binding protein Hel-NI or Hel-N2
Disclosure: Column 24-30: 65pp: English.

PT Production Column 24-30: 65pp: English.

PT Sequences given in T34454-74 represent growth regulatory protein
cDNA's which were isolated due to their ability to bind to the human
conservor specific protein. Hel-NI. The mRNA sequences corresponding to
neuron-specific protein, Hel-NI. The mRNA sequences corresponding to
these cDNA's all contained the characteristic short stretches of
neighblates found in the random RNA selection experiments (see also
trighlates found in the random RNA selection experiments (see also
trighlates found in the random RNA selection experiments (see also
trighlates found in the cDNA's isolated represented growth
countries in relading the Ark nonreceptor tyrosine kinase, the
strowth requiatory protein. No house keeping or non-growth related genes
were detected. Hel-NI was found to contain 3 RNA recognition motifs
contain stransfected into cells, the cells undergo rapid growth.

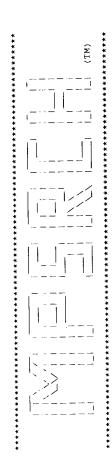
Commain is transfected into cells, the cells undergo rapid growth.

Hel-NI binds as a multimer along the mRNA, presumably enhancing its
contains instability and/or regalation for the contains for the center.
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contral nervous system; cancer; paraneoplastic cerebellar degeneration; paraneoplastic encephalomyelitis; PNP-1 octamer sequence; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      deadenylating it. This protein may be responsible for the growth cessation of neurons. Hel-N1 is an autoimmune protein in certain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Levine T;
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                                                                                                                                                                                                                                                                                       11.JUN-1995.
11.MAY-1992; 881075.
11.MAY-1992; US-881075.
15.SEP-1993; US-120827.
(UYD)-) UNIV DUKE.
Gao F, Keene JD, Levine
WPI: 96-286398/29.
                                                                                                                                                                                                                                         US5525495-A.
                                                                                                                                                                   Synthetic.
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Matches
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... urch rompleted: Fri Jan 15 00:52:25 1999
Tob time : 303 secs.

UV 1754 TAAAGTTTATGAAAAAAAAAAAAAAAAAAAA 1789 37 taaattttyttatgaaaaaaaaaaaaaaaaaa 72

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Release 3.1A John F Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd.

Fri Jan 15 00:02:22 1999; MasPar time 2651.01 Seconds 1208.482 Million cell updates/sec MPsrch_nn n a - n a database search, using Smith-Waterman algorithm Run on:

Tabular output not generated

AAAAAAAAAAAAAAAAA 1789 >US-08-955-841-1 (1-1789) from US08955841.seq 1789 CITAAGTAGACAGCIGACGA 1 GAATTCATCTGTGGACTGCT Description: Perfect Score: N.A. Sequence: Title:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 Nmatch STD: 2275026 seqs, 895388244 bases x 2 Searched.

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

genbank-sell)

jem_est1 2:em_gss1 3:em_gss2 4:em_gss3

genbank-sell)

5:qb_est1 6:qb_est10 7:qb_est11 8:qb_est12 9:qb_est13

10:qb_est14 11:qb_est15 12:qb_est16 13:qb_est17

14:qb_est18 15:qb_est19 16:qb_est2 17:qb_est20

18:qb_est21 19:qb_est8 25:qb_est4 21:qb_est5

23:qb_est7 24:qb_est8 25:qb_est9 26:qb_qss1 27:qb_qss2

28:qb_qss3 29:qb_qss4 Database:

Mean 12.038; Variance 4.488; scale 2.583 Statistics: pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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œ	Result No.	Score	Query Match	Query Match Length DB	DB	QI	Description	Pred. No.
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/organism="Mus musculus"

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ALIGNMENTS

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                     Site_2: Drail (GACCAIGTS) iste_1. Liaili (CACTSISTS).
Site_2: Drail (GACCAIGTS): Ist strand cDNA was primed with an eligo(dT) primer (ATGSSCTITITITITITITITITITITICAL double-stranded cDNA was ligated to a Draili adaptor (TGTTGGCCTANGTGS). Algasted and cloned into distinct Draili sites of the pME18S-FL3 vector (5' site CACTGTGTS, 3' site CACATGTS). NAVIS should be used to isolate the cDNA insert. Size selection was performed to exclude flagments (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTGTGCTGTAAAGGTGGG and 3' end primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 CIGGAGIIIGGGCAAGGACCIGAAGGICCIACIIGICCIGGAACIICICCAAGAIAGGCA 800
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Best Local Similarity 88.6%; Pred. No. 0.00e+00;
Matches 669, Conservative 9, Mismatches 81, Indels
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/strain="C57BL"
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11a.L. Wilkin, D. Rittner M. Redevy, P. Tound, M., Yanedda, T.,
Krizman, D., Liotta, L., Bonner, R., Schuler, G., Boquski, M.,
Powell, J., Lennon, G., Roodman, D., Hotchkiss, R., Moltzer, P.,
Trent, J., Hillier, L., Allen, M., Bewles, L., Celsel, S., Kucaba, T.,
Marran, Markin, J., Steptoe, M., Tan, F., Theising, B., Howers, P.,
Wylle, T., Waterstein, R., Wilson, R., and Plancomano, C.,
Washd-MGB/NHGRI EST Project
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This clone is available royalty-free through LLNL: contact the
TMARE consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -40ml3 fwd Er from Amersham
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Primates; Catarrhini; Hominidae: Homo.
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No. 0.00c+00; es 668; Preservative 6: Mismatches 16; Indels '
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Investing/Qualifiers
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US-08-955-841-1.rst

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Vector. -5' adaptor sequence: 5' GAATINGGACAG3' adaptor sequence: 5' CTCGAGTITITITITITITITI 3'"/db_xref="taxon:9606"
                                                                                                                                                                                                                                                          Length 608;
                                                                  /clone_"84332"
/clone_lib="Stratagene HeLa cell s3 937216"
/sex="female"
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                     /dev_stage="HeLa S3 cell line"
/lab_host="SOLR (kanamycin resistant)"
143 c 154 g 190 t
                                                                                                                                                                                                                                                        29.5%, Score 528, DB 12, 98.1%; Pred No. 0 00e+00.
                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ab40g11.s1 Stratagene HeLa cell s3 937216 Homo sapiens CDNA clone 843332 3' similar to TR.G1146129 G1146129 INTEGRIN LINKED KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 608)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Laoy, M., Lennon, G., Marra, M., Martin, J., Moore, B., Schollenborg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylle, T., Waterston, R. and Wilson, R. Wash U-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email. estiwatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Plusalable reversed clone: similarity on wrong strand
Insert Length: 1673 Std Error: 0.00
                                                      1509 GICCIBCATCITICICAAGGATAGGCACAATCAIGICAAATITGGGIGGCTITGCAGGGIC 1450
                                                                                                                                                                                                                                                                                                                                                  1389 AGGCCGAAGGCCTTCCAATGCCACCTTCAATTCCCATATTGGAGAGGTCAGCAAA 1330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 ITCATICALGCAGAICTICALGAGCITACACACATGAGGGGAAATACCTGGIGGGAIGGT 360
                                                                                                                                                                                                                                                                                                       361 AGSTOSACTS---TECANGEGACTICALICCANCICCANAITGGAGAGGICAGCAAA 417
                                                                                                                                                                                                                                                                                                                                                                                               418 GGGIACCTCCCGIGTCNACAGTTCC-ACAGAAGCACTGCAAAACTCCACATGTCTGCTGA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     477 GOSTOTESTITESTATOTICAGGGTFOGTCTGCAGAGGTTNCGGGGGGTTACCAGGCAGGTG 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                537 CATACATGCGACCANGACATTGGAACAGAACTTGACATCAGCCATGCTAATTGGGCCAG 596
                                 181 ATTOCOCCAACATGLOCOGACACTCTGGAGTTCAGGCAAGGACCTTOCAGTGCTACTT 240
                                                                                                                         241 GICCIGCALCIICICAASSATAGSSCACAAICATGTCAAATTTGGGTCGCTTTGCAGGTC 300
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Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4444 Förest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 296 1800
Fax: 314 286 1810
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High quality sequence stop: 272.
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AA485953
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vk34d11.r1 Soares mouse mammary gland NbMMS Mus musculus obna clone 9485015' similar to TP:01146129 G1146129 INTEGPIN-LINKED KINASE.
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Marral, Hiller, Allen, M. Bowles, M. Dietrich, N. Dubuque, I., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
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Vertebrata; Mammalia; Eutheria, Rodentia, Sciurognathi; Muridae;
                                                                                                      1789 IIITITITITITITITITITITITICALAARATIITAITSIGACASSCSSSSTGAIGGG 1730
                                                                                                                                                                                    1491 GATAGGCACAATCATGTCAAATITGGGTCGTTGCAGGTCTTCATTCATGCAGATGTT 1432
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                                                    41 ITITITITITITITITITITITOAAATAAACTITATIGIGACAGGOGGGGGTGGT 100
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4; Gaps
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T 31, double-stranded "fina was ligated to Eos FI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eos FI sites of the modified pT7T3 vector. PNA provided by Pr. Minoru Ko. Wayne State Univ. Library constructed and normalized by Bento Scares and M.Fatima.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Justin Totaus Mammary gland, Ventor pystypePac
(Pharmacia) With a modified polylinker: Site_1: Not 1:
Site_2: Eco PI: 1st strand obwa was primed with a Not I
                                                                                                                                                                                                                                         This obour is available royalty-free through LLNL , contact the IMAGE Consortium (info@image llnl gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            524 GCCTTGTCAGCATCTGTAACAAATATGGAGAGAATATGGAGAGAATGACTGTGGAGAAAAAGGCGC 585
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Trendents Canada R. Willam B.
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Washington University School of MedicineP
4444 Forcal Park Pathway, P.z. 9561, St. 155
                                                                                                                                                                                                                                                                                                   Seq primer: -28ml3 rev2 ET from Amersham
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John, stage*** weeks"
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                                                                                                    Contact: Marra M/Mouse EST Project
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                    Waterston, R.
The WashU-HHMI Mouse FST Project
                                                                                                                                                                                                                      Email: mouseest: dwatson.wustl.edu
                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_yref="taxon-10090"
/clone="948501"
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/ojt-"Cjgar ojam
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  Best Lonal Similarity 99 88
Matches 678, Caserrar
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                                                            Unpublished (1996)
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                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
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TOTAGE 19

GOUDE-STRUNGE CDNA was size actored. Historic EDD PD

double-strunded cDNA was size actored. Historic EDD PD

adoptors (Pharmacia), disested with Not 1 and closed into

the Not 1 and EDD ED sizes of a modified pills vector

(Pharmacia). Library went through one round of

Boardlandien to a Cot + S. Library constructed by Hento-

Soares and M.Fatima Renalde."
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National Factors Institute, Factor Geometric Anatomy Froles (1954),
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Email: Robert_Stranskerginih.go:
This older Stranskerginih.go:
This older is available trygaly.tree through LLNE, confact the
IMASE Consortiom (info@image.llm.evv) for further information.
Insert Length: 622 Std Error: 0.00
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                                                                                                                                                 604 AGCALGGCTIICTI-CACACACACIAGAGCTICTCATIACCCAGAACGAACTCAATACACAC
92E GILGUNARIDSABINDANGINASANGNASANGNASTINATIANIGANGNISTITTI STITTAGG 885
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    (base) Lo farman, Marchini, Hominidae, Homo.
    (base) Lo farman, Militain oth Patrician, Capp.

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                                                                                                                                                                                                                                                                                                   485 CACCCAACCCICAICACACACAGGGCAIAIGGCAIAIGGATCTCTCTACAACATGTTGTACAIGAA
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/tissue_type="Senescent_tibroblust"
/tachcs="thtob (ampirillin registant)"
143 c 151 a 185 t
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Pred, No. 0.00e+00;
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AI176814 697 bp mRNA EST 08-0CT-1998 EST220410 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone POVEXIS 3' end, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Rattus sp."
/note="Organ: ovary; Vector: pT7T3Pac; Site_1: EcoRI;
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                                                                                                                                                                                                                                                                                                                                         1478 ATGTCANATTTGGGTCGCTTTGCAGGGTCTTCATTGATGCAGATCTTCATGAGCTTACAC 1419
                                                                                                                                                       421 CCAATCICCATAIIGGAGAGGICAGCAAAGGGIACCICCCGIGICACCAGTICCCACAGA 480
                                       361 ACATGAGGGAAATAACTTGGTGGGATGGTAGGCCGAAGGCCTTCCAATGCCACTTCATT 420
                                                                                                                                                                                                                                                     241 GIICASSCAASSACCIICCAGICCTACTIGICTIGCATCTICTCAAGGATAGGCACAATC 300
                                                                                51 CACCATGISGUAAGISACAAAGCTCTGAGCCCGCCCTCTTGSGGCCACAGTGGTAGGGA 120
                                                                                                                                       Eukarycta, Metazza, Chordata: Vortebrata: Mammalia: Eutheria:
Rodentia: Sciurognathi: Muridae: Murinae: Rattus.
1 (bases 1 to 697)
                      Chandra, I., Mason, T.M., Quackenbush, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Institute for Genomic Research 9712, Modical Center Drive, Rockville, MD 20850, USA 1971: (301)-838-3529 Fax: (301)-838-0208 Email: nhiee@iigr.org
2: Indels

 Mismatches

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AI077857 549 bp mRNA EST 24-SEP-1998 oyllo01.sl Soares_schescent_fibroblasts_NbHSF Homo sapions CDNA clone IMAGE:1665504 3' similar to IR:013418 013418 INIEGRIN-LINKED
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                                                                                                                                                                                                                       1592 GOCTIGCTITIGGGGGGGGGGTTCCCCCAACCATGTCCGGACACCTGGGAGTTCAG 1533
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Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 549)
                                                                                                                                                                                                                                                                                   121 CAGGSAAUAAUCCCUATAACIGGGSTAGTACCATGATTAGAGAGAGGGGGGGGGGAACAGA 180
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                                                                                                                                                             1 ICATAALAAACIITAIDSESACASSOOSGETSAISSOOGGATGITOGGAGACAICAAS 60
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                                    /clone_lib="Normalized rat ovary, Bento Soares"
172 c 181 g 167 t
                                                                                                   Length 697;
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                                                                                              Ouery Match
Best Local Similarity 89.0%; Pred. No. 0 00e+00;
Matches 621; Conservative 0, Mismatches 72.
           /db_xref-"taxon:10118"
/clone="ROVBX15"
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National Canner Institute, Cander Genumme Anatumy Project (GGAE),
                                                                                                                                                                                                                                                                                        Contact. Robert Strausberg, Ph.D.
Tel: (301) 496-1150
Email: Robert_Strausberg fuil.gov
This Clone is available reyalty free through LLNL, contact the INK-17 for the Contact the INK-17 for the Contact the Contact Length of Contact the Contact the Contact the Contact the Contact the Contact for Contact the Contact Length of Contact the Contact the
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//issuc_type-"senescent_fibroblast"
//ab_bot-"uhf0# (ampfoillin resistant)"
141 c 153 q 133 t abbots
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cDNA Library Preparation: M. Bento Soares, Ph.D.
CLNA Library Arrayed by: Greq Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencina Center
Clone distribution: NOT-CARP Clone distribution information can be
found through the L.M.A.G.E. Consortium/LLMC at:
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/note-"Vertor: pl7T%P-Far (Pharmacia) with a modified
polylinker: lst strand cDNA was propared from pooled bulk
breast tomer fissue, and was then primed with a Not I -
oligo(dI) primer: Double-stranded cDNA was ligated to Ero
El adaptors (Pharmacia), digested with Not I and cloned
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
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Primates: Catarrhini: Hominidae: Homo.
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DEFINITION ALREGGGS.SI WELLEGARELBEE HONG GONS GONS GLASS (MACDELOSTON SIMILAR ES FENGILAGIZO GLASSIZO INDIGENAL FIRANCE FIRANCE EN GRASEL EL M
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Tissup Promyroment: Obristophor Meskaluk, M.D. 19.15
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High quality sequence stop: 374.
Location/Qualitiers
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/sex="female, pooled"
/tissue_type="breast"
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Email: Retwit Straus
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Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae, Motazoa, Eumetazoa, Bilateria, Coelomata,
Deuterostomia, Chordata; Vertebrata, Gnathostomata, Osteichthyes,
Sarcopterygii; Choanata; Tetrapoda, Amniota; Mammalia, Theria;
                                                                                                                                                                                                                                                                                                                                              1647 GGATGGARROA-GGTTGGGTAGIACCAIGAGGGGGGGGGGGGGGGGGAGCCAGAGGGC 1589
                                                                                                                                                      1588 IGCTGCTTTGGGGAGGTGCATTCCCCAACCATGTCCCGACACCTCTGGAGTTCAGGGAA 1529
                                                                                                                                                                                                                                 1408 AAATACCTGGTSSATSSTASSTSSAASSCCTTCCAATGCCACC-TTCATTCCAATCTC 1350
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241 GGACCTTCCAGTCCTACTTGTCCTGCATCTTCTCAAGGATAGGCACAATCATGTAAATT 300
                                                                                                                                                                                                                                                                                                             301 IGGSTCGCTITGCASGSTCTTCATTCATGCAGATCTTCATGAGGTTACACACATGAGGGG 360
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1 (bases 1 to 528)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Pifkin,L., Pohlfing,T., Soares,M., Tan,F.,
Irevaskis,E., Materston,R., Williamson,A., Wohldmann,P. and
                                                                                                  181 TGTIGGIII 9946AGGTGCATTCCCCCAACCAIGTCCCCAACCTCTGGAGTTCAGGCAA
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SP MIK2_HUMAN Q02779 MIXED LINEAGE KINASE 2',
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1289 AAACTCCACATGTGTGCTGAGGGTCTGTTTGTGTGTTCAGG 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        479 AAACTCCACATGTCTGCTGAGCGTCTGTTTGTGTCTTCAGG 519
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Source: IMAGE Consortium, LLNL
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zi24h04.s1 Soares fetal liver spleen INFLS SI Homo sapiens CDNA Clone 45,767 3' similar to IR:Gil4cl29 Gil4cl29 INEGRIN·LINKED AA677941 g22658463
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                                                                                                                                                                                                                                                                                                                                                        GACATGACTSCCCGAATTAGCATSGCTGATGTCAAGTICTCTTTTCCAATGTCTGTGTGGGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ATGTATGCACCTGCCTGGGTAGCCCCGAAGCTCTGCAGAAGACCTGAGAGACCTGAAAAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 GAATGAAGACCTGCAAAGGGACCCAAATTTGACATGATGTGTGCCTALCCTINGAGGAAG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411 AISCAGGACAASIIAGGSAIIGSAAGSINGIIGGGGGGGGGAAASSIGIGGGACN- 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotae; Metazoa; Chordata, Vertebrata, Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                 1 ACACTAGAGCCCCTCATGCAGGAGATGCACTGAATAGGGGTAGTGATGATGATGATGAGG 60
                                                                                                                                                                                                       Gaps
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Hillier, L., Allen, M., Brwles, L., Fubuque, T., Gelsel, G., Marra, M.,
Karzann, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
Theising, B., Mhite, Y., Wylie, T., Waterston, R. and Wilson, R.,
WashU-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4444 Forest Park Parkway, Box 8501, St. Louis, MO 53108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                     Longth 528;
                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      480 GGTTGGGGGGATGNAACTTCCCAAAGCAGGAGGGCTNTGGTTNGCT 525
                                                                                                                                                   Score 455, DB 16, Pred. No. 0.00e+00;
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                                                                                                                                                                                                       Mismatches
                                                                            133
/organism="Homo sapiens"/clone="195025"
                                                                            144 3
                                                                                                                                                Query Match
Best Local Similarity 96.0%;
Matches 505, Conservative
                                               <1. .>528
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(Pharmacia), digested with Pac I and cloned into the Pac I and Eco H sites of the mobiling 1977X weeter. Library went through one round of normalization. Library constructed by Pepto, Soares and M.Patima Bonaldo."
This close is available royalty-free through LANL: contact the IMAGE Consortion (infolimage lini gav) for further information. Possible reversed close similarity on wrong strand. Seq primer -4Amla twd PT from Amersham. High quality sequence stop: 450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1767 CATAATAAACITIALIGIGAGAGAGAGSSGCISAFGGGIGGGAIGTIGGGGAGAGAGAGT 1708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1529 ARGAGTIGGAGIGGIAGTIGEGGIGGALGIIGIGAAGGALAGGGAGALGAIGAIGTAAAT 1470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 TIGGGICWTIIRWCARWUICTICAITCAIGCAGAIGIICAIGAGCIIACACAIGAGGG 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GGCAAGTGAAAAGTGTGTGAAGCCGAGCGGTGTTGGGGGGGAGAGAGGGTAGAGATGAGAAAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_libe"Scares fetal liver spleen INFLS SI"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 442, DB 11, Lungth 490;
Pred, No. 0.00e+00;
0; Mismatches 9, Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (don standar 20 wook.post orporption fetye"
/lab host="PHIOR (ampidillin resistant)"
| 128 or | 136 or | 107 to 3 others
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/clone="431767"
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Best Local Similarity 97.2%;
Matches 478; Conservative
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09-FER-1995

LOCUS 159939 NAN DP WERN POUR 79429 SIMILAT TO DEFINITION yellfor SI Home Sapiens citing 79429 S. SIMILAT TO SPEMENLEHUMAN PRO192 MIXED LINEAGE KINASE I :.

RESULT 11

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vector*pBluescript SK host*SOLR cells (kanamy in fesistant)
primer* limi3 Psi*el*Bropt Psite2-xbet Normal limi3 'jornpo' from a "2
year old male Clemed unidirectionally primer olido dT Average
insert size: i.8 kb; 041 ZAP XP Ventary ' adaptor sequence:
5'-GAAIIGGGCAGGAG-3': 3' adaptor sequence:
                                                                                                                                                                                                                                                    Eucaryotae: Metazoa: Chordata: Vertebrata: Shathostomata: Mammalia; Eutheria: Primates: Catarrhini; Hominidae: Home.

1. (bases I to 52h)
Hillier, L. Clark, N. Pubuque, T., Elliston, K., Hawkins, M., Holman, M., Holman, M., Hodban, T., Homen, G., Marra, M., Parsens, J., Pifkin, L., Pohlfing, T., Ton, F., Troopskis, E., Masherston, K., Williamson, A., Wohldmann, P. and Wilson, K., Impublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This close is available toyally tree through that, , contact the IMAGE Consortium (info@image.llnl.gov) for further infommation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TAGGGATGGGGGGAAAGGGATGGAACCCATGGCTGGGGTAGTACCATGACTGGAAGGCGGGGGGGAAC
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4444 Egrest Park Darkway, Box 8501, St. Leuis, Me 63108
                                                                    human clone=79429 library-Stratagene lung (#937210)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cuery match 24.7%; Score 441: DR 5: 1
Hest Local Similarity 44.8%; Prod No. 0.006+00;
Matches 490; Conservative Amatches 490;
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/organism-"Homo sapiens"
/clone="79429"
a iso / 141 g 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
High qality sequence stops: 432
                                                                                                                                                                                                                  5'-CTCGAGTTTTTTTTTTTTTTT-3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Source: IMAGE Consortium, LLNL
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DEFINITION ab40gll.rl Stratagene Hela cell s3 937216 Homo sapiens obna clone 843332 5 similar to TE.51145129 G1145129 INTESPIN-LINKED KINASE. ;, mRNA sequence.
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[ (bases 1 to 439)

Hillier, L. Allen, M. Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lary, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wilie, T., Waterston, R. and Wilson, R. Washu'NCI human EST Project
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This clone is available royalty-free through LLNL : contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Insert Length: 1673 Std Error: 0.00
seq primer: -28m13 rev1 ET from Amersham
                                                                                                                                                                                                                     1327 GIACCICCCGIGICACCACIGACACAGAAGCACIGCACAGAGICIGGIGAGC 1268
                                                                                                                                              1507 cerecarcificicaaggaraggcacaarcarsrcaantifsssisseitiscasseett 1448
                                                                                                                                                                                                                                                                                                                                           1387 GCCGAAGCCTTCCAATGCCACCTTCATTCTAATCTCCATAITGGAGGTCAGCAAAGG 1328
                                                                                                                                                                                             301 CATICATGCAGATCTTCATGAGCTTACACACGAGGGGAAATACCTGGIGGGAIGGIAG 360
                                                                                                                                                                                                                                                                                            361 GCCGACGGGC--CAAGTGCCACCTTCAGTCCCAATCTCCATATTGGAGAGGTCAGCAA-GG 417
                                                                                                                                                                                                                                                                                                                                                                                           418 GIACCCCCCGTGTCACCAGTTTCCCCACGAAGCACTGAAAAACTCCCCAATGTCTGCTGAGC 477
                                                                                              241 CCTGCATCTTCTCAAGGATAGGCACAATCATGTCAAATTTGGGTCGCTTIGCAGGGTCTT 300
181 JOCCCCAACCAIGICCCGACACCICTGGGAGIICAGAGAAGAAGACCIICCAGICCIACIIGI 240
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                       Washington University School of Medicine 4444 Forest Park Farkway, Box 8501, St. Louis. MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
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110 c 131 g 87 t
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Location/Qualifiers
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/clone="843332"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          439 bp
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl gcv/bbrp/image/image.html
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/norgan: kidney: Vector: Bluescript SK-; Site_1:
EcoRI; Site_2: XhOI; Cloned unidirectionally. Primer:
Digo dI. Pooled kidney tumors. 5' adaptor sequence: 5'
GAATTCGGAGG 3' 3' adaptor sequence: 5'
CICGAGITTTTTTTTTTTTTTT 3' Average insert size: 1.0 kb.
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria:
Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 490)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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             1355 CCIICALICCAAICICCAIAIISGAGAGGICAGCAAAAGGIAGCIGGGGIGICACCAGII 1307
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                                                                                                                                                                                                        AA836758 490 bp mRNA EST 14-APR-1998 of37b05 s1 NCI_CGAP_Kid6 Homo sapiens CDNA clone IMAGE:1423281 similar to IR:213418 Q13418 INTEGPIN-LINKED KINASE ; mRNA
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Email: Robert_Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
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0; Mismatches 13; Indels
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/lab_host="SOLR (kanamycin resistant)"
132 c 145 g 108 t
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High quality sequence stop: 353.
Location/Qualifiers
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                                                                    THE TECACAGASCACIISCAAAAGINCAGAIGICIGGI 517
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/clone_lib="NCI_CGAP_Kid6"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Pobert Strausberg. Ph.D. Iel. (301) 496-1550
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Query Match

Matches

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Leuble-stranded CDNA was ligated to Ero RI udaptors (Pharmacia), digested with Not I and cloned into the Not I
                                                                                                                                  and Ero RI sites of the modified p77% eacher. Library went through one round of normalisation to fors, and was constituted by Rento Scares and M. Estima Bonaldo." /db_xref="taxon:9606"."
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FEFINITION 00099106 ST NTL-054FEKIDG Nome Sapieus CONA 1504 IMAGEL1574295 47
SIMILAY to TROUBATE Q13418 INFORMATINE KINASEL 1, MENA

    (bases 1 to 491)
    NT GRAP Bittp //www nebining mile gov/neicqap.
    National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

                                                                    61 GAGACACCATGTGGCAAATGACAAAATCTGAGCCCCCCCTGTGGGGANCAGTTGGTA 120
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was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not 1 -
primer [5]
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/sex+"male"
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Primates: Catarrhini; Hominidae: Home.
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Clone distribution: NVI-05AP clone distribution information can be
found through the I.M.A.G.E. Consertium/LLNL at.
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker: Site_1 Not I; Site_2: Eq. FI; 1st strand onna
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National Cancer Institute, Cancer Genome Anatomy Project (GGAP),
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Primates; Catarrhini; Hominidae; Homo.
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                                                  Score 424; DR 13; Length 439; Prod No 0.00=00; Length 439; 0; Mismatches 4; Indels
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nos 434; Conservative
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AA835033
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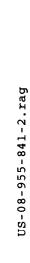
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/organism="Homo sapiens"
/note="Organ: Kidney; Vector: Bluescript SK-; Site_1:
ECORI, Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dI. Pooled kidney thunes 5' adaptor sequence: 5'
GAATICGGAGGG 3' 3' adaptor sequence: 5'
CTCGAGITTITITITITITITIT 3' Average insert size: 1.0 kb."
                                                                                           CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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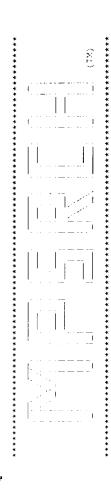
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Release 3.1A John F. Dollins, Bloompating Research Unit. Copyright (c) Loud-Lord University of Edinburgh, U.K. Distribution rights by Oxford McLeular 11d

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//notes**/Anotes**/
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                                                                                   Match
Local Similarity 30.3%; Pred. No. 4.5[0-30;
Les 79; Conservative 78; Mismatches 93; Indets 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The bresent sequence represents the constitution of the Carls protein. The sequence that encodes this protein transform plant cells. The plants overxpress the Annual cirk gene, which results in insensitivity to ethypother plants in relation to stress such as infection due to put endeteria, viruses and fundi), wound healing and soil percent
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Constitutive triple response protein.
TTP: Arabidopsis thaliama; mutant; daricultural; ethylome.
Arabidopsis thaliana.
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17-JUN-1994; US-261432.
(UYPE-) UNIV PENNSYLVANIA.
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10-AUG-1992, 928464,
10-AUG-1992: US-928464
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97-131867/12.
                                   821 AA;
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N. FSDS. 057011, 007912.

N. FSDS. 057011, 007912.

Phenotype resulting from exposure to ethylene in wild-type plants; ed. in response to states.

Plants; ed. in response to states.

A constitution of the properties of the constitution of the ethylene stand in both equation of colling and addition of the ethylene stand in both encourage of colling and addition of the ethylene stand in both encourage of colling and additional in the public colling that a nultive regulator in the ethylene stand.
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Fred. No. 8:536-30;
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R46723;
28-SEP-1994 (first entry)
Arabidopsis thallana GIRI gene product.
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                                                                                                                                          17-FEB-1994.
05-X7G-1999: U07347.
17-A73-1992: US-928464.
(TYPE-) UNIV FENUSYLVANIA.
ECKEY JY. KIEDER JJ;
WPI: 94-05555/JC.
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Best Local Similarity 29.98.
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                                                                                                                                                                                                                                                                                                                                                211 LEFLIFFHALNSFSVMIDEDMTAFI -- - SWANVKFS - FYCFGRMY - APAWVAHEALLERFF --
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This novel protein may be used to treat tumors of the CNS in a mammal by inhibiting the overexpression of the leading line of the interfering with a with a signal in a chain of signals leading to tumoridenicity.
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Leucine dipper protein-kinase, onzymo, rpk. CNS. diagnosis:
central nervous system.
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   Mismatches
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01-MAR-1994, US-205018.
(CHIL.) CHIDRENS HOSPITAL PHILADELPHIA.
Fleasure DE, Feddy U;
WFI; 95-320565/41.
N-PSDB; T01031.
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W31227 standard; Protein; 859 AA.
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E82886 standard, Protein, 859
R82886,
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   78; Conservative
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/mote- "Putative endoplasmic reticulum targeting
sequence as given in the specification"
17-FER-1998 (first entry)
Homen invertor-dipper protein kinase.
Finalis zipper protein kinase, zpk. bumar; metastasis, timour;
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Floasure D. Roddy T.
Willen Frei 1822/87.
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or protein-nucleic acid interactions involved in hyperprelification. [82, may be used to treat animals suffering from 'uncors or 'he countral kinase in vivo or by inhibiting the overexpression of leveline per persistent in vivo or by interfering with a piral should in the chain. I signals leading to tumourigenicity.
                                                                                                                                                                                                      Match 9.8%: Score 331: DB 25; Lebuth H59;
Local Similarity 32.3%, Prod. No. 3.29c-19;
Los 73; Conservative 56: Mismatches H1; Indels 16: Caps 17:
                                                                                                                                                                                                                                                                                                                                                                228 STRKSRDENE-ECPRERIESHPNVLPVLGACOSPPAPHPTLITHWMPYGSLYNVLHDSLN ____
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232 234
/note= "N-link dijecsylaries"
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(HALL) HALL INST MEDICAL RES WALTER & ELIZA,
BOYG AD. SIMPSON R. Ward ID. Wirks I. WIJ
WPI: 93-036373704
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19-THN-1992; AU3294.
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Thu Jan 14 13:43:04 1999

324 SVMIDEDWIARIS---MADVKFSFQ-C-F-GRMYAFA-WVAFEALGREFEUTHFRSAUTH T-

377 SFAVLLWELVIREVPFADLSNME-IGMKVALEGLKFILF - PGISFHVOK

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265 PILITHMANGSLYNVLHE-SINEVVPYSYAVKFALDMANGMAELHILDEFLIFNGBLUGG nifiheditvkigdiglatvksrwsgshgiegisgsliwmapevirmadkhpysfdsd.y

275 lalvtgwoegsslyhhlhlietki -emiklidiurgtaggmåjlackslihyd (%)

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Gaps 16;
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Bost Local Similarity 27:8%, Prod. No. 2 706-18;
Matches 57; Communetive 55, Mismatches 92; Indels 17; Gaps
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Disclosure: Fig 48: 108pp; English.

Disclosure: Fig 48: 108pp; English.

Presed. In a was deduced from a close isolated from a cDNA library preput. In was vicinily at All 1 and 1 a
                           Receptor type tyrosine kinase reactive with monocional antibody inches is EPH-ELK-like kinase useful for phosphorylating process in modulating pre-B, B and I cell function, in cancer
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Rest Coost Similarity 28:28: Pred. No. 5:076-18;
Matches 72; Chrestinn To Mismarches 91. Indels 20
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Sequence encoded by himan OT18 clone pHEP1-B
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R14279 standard: Protein; 515 AA.
R14279.
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Miki I. Aaronson SA, Fleming I:
HILL 91 20292/42.
N-PSDB: 010048.
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09-AUG-1990, 550035.
09-AUG-1990, TS-560135
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189..516 /label= B-raf-related gene prod

28-JUL-1989; US-386053. (USDC) US SEC OF COMMERCE. Mixi I, Aaronson SA, Fleming T; WPI; 91-073549/10.

30-JUL-1990; U04239

W09102077-A. -FEB-1991

1..188 /label= unknown sequence Location/Qualifiers

JT 9 R10932 standard; Protein; 516 AA.

P10932;

09-MAY-1991 (first entry) T18 oncogene prod. B-raf: OI18; tumour; hepatoma.

Mus musculus.

protein protein Microbio, pucon, pucon, or conning system - useful for clouding CDNA copies of edukaryotic mRNAs of all sizes and for library preparation of edukaryotic mRNAs of all sizes and for library preparation.

Disclosure: Fig 9b: 103pp: English.

Corns as deduced from a Curk.

Corns in mouse strain B6C3FL. A CDNA library was constructed in mouse strain B6C3FL. A CDNA library was constructed from a transformant. The Network library was constructed from a transformant. The Network library was constructed from a transformant. The Network library was constructed from a transformant. The Creminal portion appears to be an convenient and chicken Rmil gene prodo. There is only one AA difference, at posn. 324 where 01; is replaced by Ala in human Braft encoded protein.

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331 niflhedltvkigdfglatvksrwsgshyleqisqsilwmapevirmgikapeksilm
                                                            265 PILITHWMPYGSLYNVLHE-GINEVVLQSQAVREALDMARGMAFLHILEPLIFFHALNS
275 laiviqwoegsslyhhihiletki--umiklidiarqtaqqqqqqyha-ks:???r3-1880
                                                                                                                                                                    324 SVMIDEDMIARIS---MADVKFSFQ-G-1-GEMIAFA-WVAFBALGERFEEDTHROSENSE
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219 gtvykgkwhg-dvavkmlnvtaptpqqiqaiknevgvirktrivniilimg:20000000 105 GELWKGRWDGNDIVVKVLKVPEWSTEKSFUFNEEGFFLRIFSBFNVLPVLGACQSFPV

Query Match
Best Local Similarity 28.2%; Pred. No. 5.07e-18;
Matches 72, Conservative 72; Mismatches 91; Indels 200

516 AA;

Sequence

See also R10933.

219 dtuykakwhg-dua-kmlnutaptpqqlqafknevqvlrktrhvnillfmg-y-stk-pq 274 يع.

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(4) statylyotmiallitysninardąlitmyaraylspalskyrsnopkamkrimaecikkk 450
                          SPAVILIMED VIBEVPPADLSNME-LAMKVALERIEPTIP--PGISPHV'N-LMKICMNED 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prod. Mo. 5.076-18; 72: Mismatchee 91; Indexs 23: Saps 16;
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Fit sold Kindse and the seed to raise monoclored antibodies thich are list to immunished antibodies. The seed in this sold will be seed antibodies thich are fits unithodies my list to assect at or a diagnostic kit for the soldiester protein kindse contains on a diagnostic kit for the soldiester protein kindse contained in a biological sample.
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                                                                                                                                                                                                                                                                                                 #2527; standard: Protein: 650 AA.
#2527; standard: Protein: 650 AA.
#77-A1031902 (Lirst entry)
#77-A103 From Finase:
Protein kinase: diagnostic: monoclonal antibodies: immunisation.
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                                                                                                                                                                                                                                                                                                                                                                                                              "Aisase domain ATP binding region"
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/887 6 %
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Cytoplasmic tyrosine kinase BMX and induced INA observed of stimulate haematopoietic cell drown.

Disclosure, Page 28-29: 40pp. Endlish.

The amino acid sequence (R9458) or brosephila striker compared with the sequences of 4 members of a new backly identified non-receptor tyrosine kinase tamily. Bit (R94535) and TEC (R94536), and with brovel human cytoplasmic tyrosine kinase kamily sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 9.2%, Score 309; DH 17; Tend: 441; Best Local Similarity 26.1%; Pred. No. 4.346-17; Matches 74; Conservative 71; Mismatches 117; Indets 21; 641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 RIRPRNGTLNKHS-GIDEKOLNELIKLNENHSGELWKSHWGSN DIVVKVLKVRIMKSHKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       345 OCPGRAYAPAWVAPFALOKKPEDINRRSADMMSFAVILMELVIPE-VIPERIGIAMMER-IME 4000
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                                                    10-JUL-1996 (first entry)
Drosophila Src28c tyrosine kinase.
Sytophemmic tyrosine kinase.
Grunt growth, Deall proliferation; tymenthrent watti
Src28c.
Src28c.
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14-FER-1996 (first entry)
Protein tyrosine-kinase LpTK2.
Protein tyrosine-kinase; pTK; LpTK2; auonist; cell grewth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391 vq-rgiilekpkscakeiydvmklcwshapeerpatrvlmdqi 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label- Autophosphorylation_site
                                                                                                                                                                                                                                                                                                                                                                                       /label Tyrosine-kinase_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                              /label - ATP-binding_region.
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                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                 /label= SH3_domain
                                                                                                                                                                                                                                                                                                        65...155
/label= SH2_domain
R94538 standard: Protein; 441 AA.
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Posozg standard, Protein; 505 AA.
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04-APR-1995, U04228,
04-APR-1994; US-222616.
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WO9527061-A1.
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R41941.
PATR-4004 (List entry)
PTR yens ipin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aponist antibodies which activate specific protein tyrosino kinase(s) - also activate where proteins of kinase extracellular domain and 19 constant 35mush. Assist in studying, and therapeutic modulation of cell growth and differentiation. Dis protein the constant is a differentiation of selection of the tipp, English. Dis protein based on protein tyrosine-kinase (FTK) sequences were used to scient about the constant in the constant growth years and the constant in the constant (to be a magakaryogita sell the constant of the design drugs that modulate pTK kinase pTK. And one key assist to design drugs that modulate pTK
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In Gardan-ST and R41897-02.

The LPIRs are offers in limphorating folia as well as metallicity and intrinstructure of the limbhoration in the partial and intrinstructure associations. The protection as equence courses, to Q45749 is claumed (claum.) and stated as given in the specification, however is missing from
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Coal Similarity 26:18, Frod. No. 2:206:17; Tedols 18.
c cs. Conservative 70. Mismatches 107, Induls 18.
                                                                                                               Lee JM, Matthews W, Isai SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-A00-1993
22-JAN-1993: UUUSES.
22 JAN-1992: US-EE8925.
(NUML) NEH ENGLAND DEACONESS HOSTITAL.
PPI: 93-320330/40.
NPI: 93-320330/40.
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(SETH ) GENENTECH INC.
Bennett BD, Goeddel D,
Wood WI:
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08: T03097.
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Best Local &
Matched
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                                                                                                                                                                                                                                                    229 idrosigilkrigsgqfgorweglwnnttpranktik-pg-sm-dprdilrusgiranir 285
                                                                                                                                                                                                                                                                                                                      198 IPENQLNELIKLNENHSGELWKGRWYGND-IVVKVLKVRDWSTRKSRDFNEECPRLRIFS 246
                                                                                                                                                                                                                                                                                                                                                                                            286 hpkliglyavo tledp lyiitelmrhgslyeylqnd graitlydydmaaqvasqma 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307 FLHT----LEP-LIPRHAL-NSRSV-MIDEDMTARISMADVKFSFQCPGRMYAPA-WVAPE 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 ALQKKPEDTNRRSADMWSPAVLLWELVT-PEVPFADISNMFIGMWVALEGLRPTIPPGIS 💠
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Rest Local Similarity 28.2%: Pred. No. 6.25c-17:
Matches 75; Conservative 70; Mismatches lui: Indels 20:
                                                                                                     Score 311; DB 8; Length 505;
Pred. No. 2.20e-17;
70; MismatChes 107, Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-forminal truncated cytoplamic tyrosine kinase. cytoplasmic, tyrosine kinase, blood; cell differentiation: screening; anticancer agent; SH3; src homelogy domain.
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871132,
27-0d1-1995 (first entry)
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                                                                                                            Sucry Match
Best Local Similarity 26.1%;
Matches 69; Conservative
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29-MAR-1994; JP-058553.
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                                          505 AA;
the publication
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N-PSDB; Q84888.
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                                          Seguence
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Bost L. Similarity 28:28: Prod. No. 6:256-17;
Marthes TE: Conservative 70: Mismatches ICL Indels 20: Gaps 17;
215 entvetjavil-hypaty-lumch-vskanivnfirtraralymtagliafsibvacamcy 301
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                                                                                    LITE ENVIS VIOLET CHINTERTH LIBET CONTINUES CHE VVDOSOAVE ALDRARGMAF 307
                                                                                                                                                                                                                             **4 KPHTTHRESALAMSFAVLLMBILL* UPFADILSNMEHGMKVALEGIRPT (PPG1SPHVC 422
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Scarch completed. Wed Jan 13 12.18.21 1999 Job time : 59 secs

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Release 2.1A John F. Collins, Blockming Research Unit. Copyright (c) leaseless Hoperstry of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd.

MPsych_pp - protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Jan 13 12:15:35 1999; MasPar time 19.78 Seconds 855.755 Milion cell updates/sec Tabilar output not generated.

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Searched: 116095 segs, 37457910 residucs Post-processing. Minimum Match 0% Listing first 45 summaries

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Pred. No. is the mader of results preditted by chance to have a score greater than or equal to the score of the result being printed, and is delived by analysis of the total score distribution.

Mean 49.323; Variance 105.679; scale 6.467

Statistics:

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ALIGNMENTS

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b) a negative regulator of the ethylene response pathway
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### Protein-tyrosine kinase (EC 2.7.1.112) + - freshwater spens (Spongilla lacustris) (frament)

**Congilla lacustris) (frament)

**Formal_name Spongilla lacustris
07-may.laga **Sequence_revision 07-may*!aga **Lext_channer
08-Sep-1997
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ATP: phosphotransferase; tyrosine-specific protein kinase.
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28-Sep-1990 #sequence_revision=2H-Sep-15-6- #formal-19-6-1997
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Mol. Cell. Biol. (1990) 10:3578-3583
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#journal Moi. Cell. Biol. (1988) 8:843-853
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                                           357 APE-A-1Q-KKPE----DINPPSADMWSFAVILWELVIREVPFADISNMEIGMKVALEGI 409
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Gilardi-Hebenstreit, P.; Nicto, M.A.; Frain, M.; Mattei, M.G.; Chestier. A.: Wilvinson, D.G.; Charnay, F.; Uncogene (1992) 7.2491.2506
An Eph-related receptor protein tyrosine kinuse acceptor protein acceptor protein the developing mouse hindballs.
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##Cross-references BMR: X$7242; NID:q$3189; PID:q$3190
IFICATION #superfamily protein-tyrosine kinase src: Drotein kinase
homology: SH2 hamalogy: SH3 homology
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Blochem, Biophys Pes, Commune (1994; 20216) 662
Clouing of a novel putative protein kinase having
                                                                                          ##molecule_typc mRNA
##residues 1-450 ##label RES
##cross-references EMBL:005247; NID:9452471; PlD:0452472
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29:58: Pred. No. 2.176-35;
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#cross_references MUID:94195789
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Obery Match
Best Local Similarity 20:3%, Prof. No. 1.456-35,
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J. S.ool. Chem. (1994) 279 36765 30817
Jenilfication, molecular cloning, and characterization of dual leucine 2pper bearing kinase. A novel serine/line-order profess kinase that defines a second subfamily of mixed lineage kinases.
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Puebsamen-Waigmann, H.
Proc, Natl. Acad Sci. C. A. (1901). #3:10411-10415
Two additional protein-tyresine kinsees expressed in human lung. fourth member of the fibroblast growth factor receptor family and an intracellular protein-tyresine
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247 HENVERVIGACOSPPAPHPILITHWMPYGSLYNVEHBERNYGGGAVABALLHARFIMA (C. F.
                                                                                                                                                                *Superfamily proteintyrosine kindsesses progresses benedogy, SH2 homeledy, SH4 homeledy
benedogy, SH2 homeledy: SH4 homeledy
ATP, autophosphorylations phosphoprofein; [68]
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Elochim Biophys A-1; (1993; 1172;200-204
Cloning and characterization of a novel member of protein
Kingse family from Soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304 VERS-NNEVHED-LAARNYLVSEDNVAKVSDEGLIKEASSTED GKL-FVKWIAFRAGER
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protein kinase K (FC 2.7.1.-) Soyteons
#formal_name Glycine max #renmmen_name Soyteon
13-Jan-1995_#sequence_revision if Jan-1995_#rext_chanse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 ALINMKELKLIQTIGKGEFGDVMLGD/FRONKVAVKTIK-NI ATH ALAHTAFALTE
                                                                                                                                                                                                                                                                                                                                                                                              9.68; Score 324; DH 1; Legath 45; 99.68; Pred. No. 2,39c-44; tive 67; Mismatches 98; Indois 5
                                                                                                                                                                                                                                                       #domain SH3 homology #131%; vgs.
#domain SH2 homology #131%; vu.v.
#domain provide Vinase homology #131%; kt.v.
#leqion provide Vinase Arterbinding kt.v.
#active_site Lys #status prediction
#length 450 #molecular-weight for46 #supenger
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Best Local Similarity 28.59; Prof. Mo. Lithing.
Matches 78; Conservative 65; Mismaropes 11; Labels 17;
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##cross-references EMBL:M67449; NID:q170944; FIREN176:47
                                                                                                                                                                                                                            tyrosine-specific protein kinase
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nes 76; Conservative
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$29851
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ints engine is refrect in regulating cell function in the muscolloskeral system, and in the mitogen activated pathway in the fracture healing.
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Rest Loval Similarity 21.9%. Pred. Mo. 1.600-34,
Matches 71. Constructive 57, Mismatches 81, Indels 16, Gaps 15;
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#domain Kinase calaiytic *status predicted *label CAIN #domain Kinase calaiytic *status predicted *label CAIN #could protein linase NTP-Ending #colf.
#region leading Zipper motif.
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151 VURA LIIGURGAROAROAN MOVYKEBAVAVKIIMVEER ONGALASFIEKTEREVII DIG
                                                                      188 LDARGERSTEINGERSTEINFEWERWICHTEN FOR THE WEITH SETRIEBER 241
                                                                                                                                                                                                                                                                                                                                                        100 ARGRETIRA DVIRKO (MIRALIMEDNRIMIATACEGIACEEASCILLACTIGINYRWMA 306
                                                                                                                                                                              530 ICTMENTINGISILÖHRINHINNETSCHNINGILLI ON AMERSONNO SKIANGSSONS
                                                                                                                                                                                                                                                242 LRIFSHPNVLLYVLGAGGSPRAFHEITINWAFYGSLYNVLHEGINFVVTGSGAVFFALDM 201
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dual leache zipper Kinase (EC 2.7...) - rat

*formil_ease Bailis hithuiling frommon_name Norway rat
07-011-1997 *sequence_revision 18-Jul'1997 *text_change
17-Jul-1998
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The Eck receptor tyrosing kinase is implicated in pattern formation during gastrulation, hindbrain segmentation and limb development
                                                                                                                                                                                                                                                                  Ganju, P.; Shigemoto, K.; Brennan, J.; Entwistle, A.; Reit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##GCOSS-references EMBL:X78339, NID 4505294; FID 4505287
##note the nucleotide sequence was submitted to the EMBL ::
Library, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 IVVKVLKVPPWSTPKSPERNEEGPFFFFFFFFWLPWLPWLGAGGSPPAPHFTLITHWAPYGS 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE LEMETERENDESESV-L-CINGMERGIASSMANIANARH THRED LAARMIINTENIIGEN TER
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                                                                                                                                 #formal_name Mus musholds # homeor_name Nouse mouse 07-May-1995 #sequence_revision 21-191-1995 #rext_change 29-May-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gliardi-Rebenstreit, P.; Nieto, M.A.; Frain, M.; Mattor
M.G.; Chestier, A.; Wilkinson, D.G.; Charnay, F.
Cheogene (1992) 7-24-5-556
An Epk-related remeta: pritch firsting birate gene
segmentally expressed in the developing mouse bindbr.
330501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      757 SDF3LSPVLEEDPEATYTTS-GGRIFIPWTAFFALSYRKFTSASDVWSYGTVAGTAA 000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              816 ERPYWELSNHEV-MKAINDGFPLPTPMF@PSAIY@LMM@GW@@ERSFPPKFALTVSILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

9.5%, Score 324, DB 2: Length 977:
Best Local Similarity 28.5%; Pred. No. 2.39e-34;
Matches 59, Conservative 64; Mismatches 91: Indels 17:
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Mcan 50,761; Variance 89,841; scale 0.565

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SUMMARIES

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ALIGNMENTS

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THISTORY BENCH SERVINGS AND ADULI FLANTS.

-1 TISSUE SPECIFICITY: EXPRESSED IN BOTH SEEDLINGS AND ADULI FLANTS.

-1 CIRI MUTANTS DISPLAY ETHYLENE-TREATED PHENOTYPES, RESULTING IN PLANTS WITH SMALL, UNEXPANDED LEAVES AND WHOSE SEHD COTYLEDON OF SMALLARIY: WITH THE CONSEPVED CATALYLIC DEMAINS HE SHE/THR-PROTEIN KINASES, BELONGS TO THE MIL/RAF SUBFAMILY.

REMBL: 108789; G166680; ---

REMBL: 108789; G166680; ---

REMBL: 108789; G166680; ---

REMBL: 108790; PROTEIN KINASE_ATF, 1.

REMSL: 108790; G166680; ---

REMSL: 108790; PROTEIN KINASE_ATF, 1.

REMSL: 108790; PROTEIN KINASE_ATF, 1.

REMSL: 108790; PROTEIN KINASE_ATF, 1.

REMSL: 108790; REMINERARE ENTINE REMSL: 108790; PROTEIN KINASE, ATFRINING.

REMSL: 108790; PROTEIN KINASE_ATF, 1.

REMSL: 108790; REMINERARE ENTINE REMSL: 108790; PROTEIN KINASE, ATFRINING.

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REMSL: 108790; PROTEIN KINASE_ATF, 1.

REMSL: 108790; REMINERARE ENTINE REMSL: 108790; PROTEIN KINASE, ATFRINING.

REMSL: 108790; PROTEIN KINASE_ATF, 1.

REMSL: 108790; PROTEIN KINASE_ATF, 1.
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MEDLINE; 93161417.
KIEBER J.J., ROHENBERG M., ROMAN G., FELDMANN K.A., ECKER J.R.:
CELL. 72:427-441(1993).
-:- FUNCTION: ACTS AS A NEGATIVE REGULATOR IN THE ETHYLENE RESPONSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D->E: IN CTF-1: EXHIBITS ETHYLENE-
TPEATED PHENOTYPE.
ED4-02920 CPG32;
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                                                                                                                                                                                                                                                                                                    AFRES).
BURANCIA: PLANIANA (MOUSE-EAP CPRSS).
CAPPARALES: CRUCIFERAE.
CAPPARALES: CRUCIFERAE.
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PPOLEIN KINASE.
AIF (ET SIMILARITY).
AIF (ET SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
P-X: IN CIRI-4, EXHIB
                                                                                                             01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
SERINE/THREONINE-PROTEIN KINASE CTP1 (FC 2 7 1 37).
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                              821 AA.
                                       PPT;
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                                       STANDARD;
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1LT 1
CIR1_ARATH
Q05609;
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BINDING
ACT_SITE
MUIAGEN
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                                                                                                    194 LINFIERINGNESSELWRGEWIGNDIVVKVLKVERMSTEKSKLENEEUPRIRIFSHPNVL 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --SNEKS-DVESEGVILWELATLOOPWGNLNPAQVVAAVGFKOKPFEIPHNINPGVAALI 784
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(1.6%; Prod. No. 9.916-54;
native 61: Mismatches 106; Indeis 17: Gaps 14:
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FINANCIAL DESCRIPTION (SLIME MODE).
FINANCIAL DESCRETA SARONASTINOPHORA SARONANA RHIZON DA)
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-N V-194 (REIL 14, LAST SEGÜENCE CEDATE)

-N V-1944 (REIL 12, LAST SEGÜENCE CEDATE)

-N V-1944 (REIL 12, LAST ANVOIATION FETATE)

-N V-1944 (REIL 12, LAST ANVOIATION FETATE)
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417 AA: $12
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PIPE BEGGTO, RESSTO
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358 PEALOKKPEDTINRRSADMWSFAVILMELLVIREVOERALLSHIREFIRAKVALA (LEPTING) (1.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307 FIRTLEPLIPRHALNSRSVMIDE-DM- TARISMADV-KFS-FORT-GRMYAFAVAVALEA ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 ALYNRE-TIK-S-DVWSFGVLISELVIHGRMPYPGMINKOV LEAVEFOFFRMFTETTIL . . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 TOKKPEDINRESADMWSFAVLLWELVTRF-VPPARASONBESOMKVALISOLIPTIOPGIST 4 FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 HPNVLPVLGACOSPPAPHPTLITHWMPYGSLYNVLHEGINEVVINGSGAVKFALLNIAREMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 HPNLLQLYAVG-TIGEP-IYIVTELMKYGSMLFFIKHGEGKNITLH, MV7MSK, LASSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 IDRITIQLQRKLGQGNEGEVWAGVWNSITAVAVKTLK-POHTIPEVKDFVLGALVGAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE, PSSOO1: PROTEIN_KINASE_IPM:
PROSITE; PSSOO01: SH2; 1
TRANSPERASE: TYPOSINE-PPOTEIN KINASE ATPPIN: NB: SH2 1- WAYS
NOW TER 1
DOMAIN <1 1
DOMAIN KK -12
ND F-12
ND F-13
ND F-14
ND F-14
ND F-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UFLATE)
01-NOV-1995 (REL. 32, LAST SEQUENCE UFLATE)
TYROSINE-PROTEIN KINASE SERN (FI 2.7.1.112) (FEA ARINE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 29.9%; Pred. No. 6, 52.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 5,530-48;
63; Mismatches 106; [mpo./s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
W: 7864FB9R OPC42.
                                                                                                                                                                                                                     4 44 AA.
                                                                                                                                                                                                                                                                                                                                                                 SPONGILLA LACUSTRIS (FRESHWATER SPANGE).
EUKARYOTA: METAZOA: PORIFERA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE: PS00107: PROTEIN_KINASE_AIP; IPROSITE: PS00109; PROTEIN_KINASE_AIP; IPROSITE: PS00109; PROTEIN_KINASE_IYP; IPROSITE: PS50011; PROTEIN_KINASE_IPROSITE: PS50011; SH2; I
                                                336 DPELKLLLIQCWEADPNDRPPFTYIVNKL 464
                                                                                              418 SPHVCKLMKICMNEDPAKRPKFDMIVPIL 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                PRT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              420 HVCKLMKICMNEDPAKRPKFDMIVPILE 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 280 7TP 7TP 7TP 94 94 94 94 94 94 9186 BY 334 AA; 37880 MW; 7
                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                              SRK3_SPOLA
P42689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SULT 4
KYK1_DICDI
P18150;
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BINDING
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PRT: 1584 AA

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1345 ARBAYVOLDADIAGUST MICHATSANAGASTASTAFITI HENGLEDAR HENNAGATARIA (471)
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OTHER TO THE STATE OF THE SECTION OF THE SECTION OF THE STATE OF THE SECTION OF T
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29.48, Ered. No. 1.466.47;
40.00, 10.00, 10.00, 10.00;
                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CHIO;
NOCKCLES G.M., SPUDICH J.A.;
SOBHLIED [ANT-147] H. MAR, BREANFILET DAIM BANKS.
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I (IN REF. D).
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Rest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM M.A.
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4F] VITPEF-PF-TILLEFXSHONLDFLFSAGSETDAVALLYMATGASGKSTLESSKYIH 5 T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256 ACTSPPAPHETLITHWMPYSSLYNVIHESTNFVVTSSQAVFFALDMARGMAFLHT---LE *1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 KIDSSQYGEVYEAVWKPYGNIVAVKILK - ELITMALKITT FRAATMYEHRHUINGLID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POSINE-PPOIEIN KINASE, ANF-EINDING, PROSERRADI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Socre 340, DE 1, Length 152%
Pred. No. 4.96e-45;
62, Mismatches 99, Indels 21:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           GERTLER F.B., HOFFMANN F.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOPEWANN F.M. FRESCO L.D., HOFEMAN-FALK H., SHILO B.-Z.: CELL 35934-401 (1988).
-!-CATALYLIC ACTIVITY. AIP . A PROTEIN TYPOSINE = ADF -
PROTEIN TYPOSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIP (BY SIMILABILY).
AIR (BY SIMILABILY).
BY SIMILABILY).
PHOSPHOPPLATION (AUTO-) (BY ESST - VOYV (IN PER 2).
MW. AEBBILF (EFICE).
1523 REFIPLISSKWKEILIQOWDSNEDSRETEKLITVHIKEMED 1564
                                                  410 PPIIPPGISPHVCKLMKICMNEDPAKPPKFDMIVPIIFKMQD 451
                                                                                                                                                                                                                                                                                                                              CROSOFETLA MELANGGASTER (FRUIT FLY)
EUKAPYOTA, METAZOA, ARTHROPODA: INSECTA: DIPTERA
                                                                                                                                                                                               21-JUL-1996 (REL. 01, CREATED)
01-OAN-1990 (REL. 13, LAST SECUENCE UPDATE)
11-OAN-1995 (REL. 32, LAST ANNCATION UPDATE)
12-SOSINE-PROTEIN KINASE DASH/ARL (EC 2 7 1 112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN KINASE.
                                                                                                                                                  FPT. 1520 AA
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MOL CELL BIOL 8:843-853(1988).
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Best Local Similarity 30.7%;
Matches 81; Conservative
                                                                                                                                                    STANDARD
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204 265
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MEDLINE; 88174728.
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SH2 DOMAIN;
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                                                                                                                                                                                         FESAL MWSFAVILNELVIBEN FFAM SHHELDHRYDLEGIRFFILFF HSFBA IKLMKIG 428
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HILELD AND ALL STANTABLE STANTABL
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PHOSPHORYLATION (AUTO-) (EN SIMILARITY).
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-1- STRING. AS WELL AS IN HOUNTAIN BRAIN.
-1- STRINGE STRINGE STRINGE STRINGE STRINGES IN THE DATALYTIC
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NYCHER A., WILKINSON D.G., CHARNAY P.;
NYCHION, SHECHELOALLY HOSPHORYLATES A TYPOSINE ON THE SKO KINASE, IHIS LYROSINE ACTS AS A NEGATIVE REGULATORY SITE.
CAN A S. ACT ON THE LYROSINE ACTS AS A NEGATIVE REGULATORY SITE.
TANANCHI M. THE LYROSINE ACTS AS A PROTEIN TYROSINE - ADP -
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[KARY 1A: METAZEAL GHORLATA: VERIEBRATA: IETRAPODA: MAMMALLA:
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KLAGES S., ADAM D., CLASS K., FARGNOLL J., BOLEN J.B.,
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No. 6.216-43;
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48; Indels 16; Saps 13;

THE ALMARGICACION CONTROPORTATION OF THE STANDARD MANAGER 244

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361 KKEST--KS-DVWSEGILLWEIYSFGRVPYPRIPLKHVVPHVE KOVKKEALFFFFAVY 41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SPOUDNOE OPHRATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
EPHRIN TYPE-A RECEPTOR 3 PRECUESCE (EC 2.7.1.112) (IYETSINE PPOTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-SPRACUE-DANLEY,
LI Y.Y. ACTIFERNAN C.F., FELDMAN A.M.;
SUBMITTED (DEC-1996) TO EMBL/GENRANK / DIRT FATA PANKS.
FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY.
FUNCTION: A.A. AND -AS.
-!- CALALYTIC ACTIVITY: ATP - A PROTEIN FYR-SINE ALF.
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- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
- SIMILARITY: TO OTHER PROTEIN-TYPENINF FINASEE IN THE ADALY.
- DOMAIN. BELONGS TO THE EPHRIN PECENTOR FAMILY.
- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE ITLIBET PROFINS.
                                                                                                                                                     247 HPNVLPVLGACOSPPAPHPTLTTHRESTYCKLERWIEL GLARVVER, SLAVKEALTRESTAGES
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PROSITE: PS00107; PROTEIN_KINASE_ATP;
PROSITE: PS00109; PPOTEIN_KINASE_ATP;
PROSITE: PS00109; PPOTEIN_KINASE_TYR;
PROSITE: PS00791; PPOTEIN_KINASE_TYR;
PROSITE: PS00791; PPOTEIN_KINASE_TYR;
PROSITE: PS00791; PPOTEIN_KINASE_TYR, N.V.
TRANSFERASE; TYROSINE-PROTEIN_KINASE;
PROSITE: PS01186; ESF_2; UNKN.WN.];
PROSITE: PS01186; ESF_2
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EUTHBRIA: RODENTIA,
                                                                            245 HSNLVQLLGVIVEEKGGL-YIVTFYMARGSLVIYLBSR 18-VULTV-112-RI-11.
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187 GIDFKOLNFLIKLNENHSGELWKGRMGGMDIVVKVIKVFIKST9ksen nga
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DPHRIN TYPE-A RECEDICY (
PXTRACELLULAR (PUTINITAL).
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CYS-RICH.
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MEDLINE, PARANASHI Y., YAMANIC T., NARAGAWA H.:

J. KAPA M. NADA S., YAZANASHI Y., YAMANIC T., NARAGAWA H.:

J. KOLL, CHEM. 166.24249.24502(1941)

J. FUNCTION. SPECIFICALLY PHOSPHORYLATES A THROSHED CN THE FINANCE. THIS TYNOSINE ACIS AS A NEGATIVE REGOLATION ON ALSO ACT ON THE LYN ANTENNEYS CAN ALSO ACT ON THE LYN ANTENNEYS CAN ALSO ACT ON THE LYN AFFORMSES.
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                                                                                                                                                                                                                                                                                                                                                                                       01-001-1993 (REL. 27, CREATED)
01-001-1993 (REL. 27, LAST SEQUENCE UPDATE)
01-NY-1995 (FEL. 32, LAST ANNIANTIN THIMFY)
11805INE-PROTEIN KINASE CSK (EC. 2.7.1.112) (1-480 KINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NADA S., OKADA M., MCAULEY A., COOPEP J.A., NAKAGAWA H.:
NATUPE 251:69-72(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHE
PROTEIN KINASE.
AIP (BY SIMILARITY).
AIF (EV SIMILARITY).
BY SIMILARITY).
FHISHAFYTY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atch 9.6%; Score 324; DB 1; Let sal Similarity 29.6%; Fred No. 1.118-41; 76; Conservative 67; Mismotches 98;
                                                                                                                                                                                                                                                                                                                                     450 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE: PSO0107; PROTEIN_KINASE_AIP: 1.
PROSITE: PSO01109; PROTEIN_KINASE_IYB: 1
PROSITE: PSO0011; SH2; 1.
PROSITE: PSO0015; SH2; 1.
PROSITE: PSO0015; SH3; 1.
TPANSTERASE_IYB: PSOO015; SH3; 1.
TPANSTERASE: TYPOSINE: PPOTEIN FINASE; ATTRACTERASE; ATTRACTERASE; ATTRACTERATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE; 91226538.
                                                                                                                                                               250 AMERICSDOLKEOPEEPPEETEATIELL 280
                                                                                                                                                                                                                       421 -VCKLMKICMNEDPAKPPKPDMIVPILEKM2 450
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222
314
314
416
50746 MW:
                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RATIUS NORVEGICUS (RAI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S15094; S15094.
HSSP; P41240; 1CSK.
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2222
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4415
50 AAS
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MYC_FES
SEQUENCE
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BINCING
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| TSK_FAT
| F32577;
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* 4 YLET-NNEVERL-LARENTLYREDWARVSLEGELEFASSIODIGKL-PVKWTAFFALKE 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (4) KKEST KK LVWSBGILLMELYSBRIRVDYDDJBT MAVVDDVBLPTTPVF 711.1381AVF 416
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PRICE 450 AA.

TERRITORS (REL. 4) CREATED)

TERRITORS (REL. 4) CREATED)

TERRITORS (REL. 4) LAST SECUENCE UPDATES

TERRITOR (PAT ANNOTATION UPDATE)

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MADOLINE: POSSORIA:
FARTANEN DEL ARMSTRONG ELL BERGMAN M.L. MAEKFLAE T P.L. HIDVINEN H.L.
HTERNER ALL ALLIALO K.J.L.
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STREBHARDT K PHERSAMPHIMAN TRANS
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FURANCIAS METANOAS CHEROATAS VERTERRATAS TETRAPODAS MAMMALLAS
FUTHERTAS PETMATES.
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WITHERA A.E.R., RAIRING M., ZEBLEN J.P., CORRINGING S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MENTINES (2 34.2)
PRABITION NEW ALT BOLIETTBOLL STREEHARDT KOUTERSAM
FELL MINES ALT BOLIETTBOLL STREEHARDT KOUTER (1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417 IVMKNOWHIDAATRPIE 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 * MINEL TANDITANE 4 44
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BY SIMILARITY.
PROSPHORYLATION (AUTOO) (BY SIMILARITY:
40307909 OROTA)
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001145: 062212;
001-007-1994 (REL. 30, CREATED)
01-007-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UFDATE)
EPHPIN TYPE-A PPCEPTOR 2 PPE"*FSOR (ES 227 1112) (TYP**SINETED TANASE RECEPTOR ECK) (EPITHELIAL CELL KINASE) (MIK***)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE 9309648.
GILARD-HEBENSTREIT P., NIETO M.A., FRAIN M., MATTEL M. G.,
CHESTIER A., WIKKINSON D.G.,
ONCOGENE 7.2499-22961192.
I. FUNCTION. RECEPTOR FOR MEMBERS OF THE BYBLIN-A FAMILY. HINSS J
EPHRIN-AL, -A3, -A4 AND -A5, MAY FUNCTION IN DISTINCTIVE ASPECTS
OF PATTERN FORMATION AND SUBSEQUENTLY IN DEVELOPMENT F. SEVERAL
                                                                                                                                                                                189 ALNMKELKLIOTIGKGEPOPVM OTVETVEVAVE OF NO AT ADAPTABASSUELLE
                                                                                                                                                                                                  FETAL TISSGES.
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE * ADP
-- PROTEIN TYROSINE PHOSPHATE.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PHOTEIN.
-!- SIMILARITY: TO OTHER PROTEIN TYROSINE KINASES IN THE "AIALYTH"
                                                                                                                                                                                                                                          245 HSNLVOLLGVIVEEKGGL-YIVTEYMAKGSLVBYLRBEGRSVLGBYLLEKFSLLV " ED-
                                                                                                                                                                                                                                                                   247 HENVLEVISANOSPPAPHPTLITHWKFYGSLYNVLAHENTWYN, SLAVK) ALL NACH GE
                                                                                                                              9-64: Score 244 LB Liberal B-46::
29-68: Pred. No. [115:44];
ative 64: Mismarches 97: [164:18-19:]
                                                                                                                                                                                                                                                                                                304 YLEG-NNFVHKO-LAARNVLVSERNVAKVSRERILEEASSTGETREL FURKLA.
                                                                                                                                                                                                                                                                                                                                                        361 KKFST--KS-DVWSFGILLWEIYSPGFVPFPPELGLIVVPFVFF KOFKMOAR II
                                                                                                                                                                                                                                                                                                                            307 FLHTLEPLIPRHALNSRSVMIDEDMTARIS-MADVK--FSFOCPGHMYAFANVS
                                                                                                                                                                                                                                                                                                                                                                                   364 KPEDTINRSADMWSFAVLLWELVTRF-VPFADLSNMFTOMKVALEKLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O CHARNAY P. COTTABLE FOR THE FORMAT P. C. CHARNAY P. COTTABLE FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHIGEMOID K., BRENNAN J., ENTWISTLE A., PFITH A.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUS MUSCULIS (MOUSE).
EUKARYOTA: METAZOA: CHOPDATA: VERTEBRATA, TETHAPITA: BUELLE
                    SH2.
FROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (br SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
SEOURCE OF 552-977 FROM N.A.
STRAIN-C57BL/6; TISSUE-EMBRYO;
MEDLINE: 95044306
BECKER N., SELTANDOU T., MIRCHAY D.
NIETO A., WILKINSON D.G., CHARNAY P.,
MECH. DEV. 47:3-17(1994).
                                                                                                    50704 MW;
                                                                                                                  Ouery Match
Hest Local Similarity 29.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 742-799 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                417 EVMKNCWHLDAAMRPSF 433
                                                                                                                                                                                                                                                                                                                                                                                                                                          423 KLMKICMNEDPAKRPKF 439
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                171
204
209
209
314
416
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  SEQUENCE FROM N.A. MEDLINE: 94239737. GANJU P., SHIGEMOTIC
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MOD_RES
SEQUENCE
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MEDLINE; 94195789.

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17; Saps 16,
                                       PROBLEM X10-20 JUGGEOT STREETH THE III-LIPE D'HAINE BENEL X10-20 JUGGEOT STREETH D'HAINE BENEL X10-20 JUGGEOT STREETH STREETH D'HAINE BENEL X57-04-3 GESIGOT STREETH S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OL IDRILIBERLGEFEV-T-ILVSKIFFIRSCRRYLANKN-YVBPD-LAAFNILVNSNLVCRV 756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRUSPHUKILATION (ACTO-, (EY SIMILARITY)
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHOPPATA: VEPTEBBATA: TETFAPODA: MAMMALIA:
DEMAIN, BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILANIII, CONTAINS I PIBECHECTIN THE III-LIPE TOWAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O March Court (Second Description Court (Second Second Sec
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OTTERFIGES (RRL. 33, LASI SEQUENCE UPDATE)
ISJULISSE (REL. 39, LASI ANNOTATION UPDATE)
MEGANNUMIERASELINING INRUSINE FEOTEIN KINASE (EC. 2)
UTBASINE TRUCKLIN KINASE CIK) (FROIELN KINASE NIK).
HARY OF CIV OF NIY
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SPHRIN TYPE-A RECEPTOR 2.
SNIRACELLULAR (POTENTIAL)
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AIP (BY SIMILARITY).
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POIENTER. 2).
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TISSUE-BRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD:
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EURABYOTA: METATOA: OF
EUTHERIA: RODENTIA.
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STRUCK STORY STORY
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-:- TISSUE SPECIFICITY: MOST ABUNDANT IN BPAIN, AND TO A LESSER EXTENT IN THE SPLEEN, THE THYMUS AND THE LIVER. ALSO FOUND IN THE I-CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 IDLYHLTLGAÇIĞBĞERSAVLÇSEXLƏŞKVAVKNIKÇESENDE YERÇETLDETATOTKLÇB 1883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --- ALTERNATIVE PRODUCTS: BY ALTERNATIVE USAGE OF 2 JUXTAPOSED SELECTED ACCEPTOR SILES, A SECOND. LESS ABHIDARY PRODUCT IS FORNO.
--- SIMILARILY: TO OTHER PROTEIN TYROSINE KINASES IN THE CALABITY DOMAIN. BELONGS TO THE OSK SUPPAMITY
---- SIMILARILY: CONTAINS I SH2 DOMAIN.
---- SIMILARILY: CONTAINS I SH2 DOMAIN.
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Pred. No. 7.57e-41;
69; Migmatches 99; Indels 20; Gags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPOSINE-PROTEIN KINASE; AIP-BINDING: SH2 DYMALN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 FNLVRLLGVIL-HHGLY-IVMEH-VSKGNLVNFLPTRGRALVSTSQLIQFALGV.
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ATP (BY SIMILARITY).

BY SIMILARITY).

BY SIMILARITY (STATEMENT).

To by (IN REf. 2).

To fo (IN ALIERNATIVE FORK).

1100E895 CHC32:
                                                                                                                                                                                                CHOW L.M.L., JARVIS C.D., HU Q., NVE S.H., GERVAIS F.G., VEILLEITE A., MAIIS L.A.;
PPOC. NATL. ACAD. SCI U.S.A. 41.4475-4474(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: ATP + A PROIEIN IYROSINE = ADF + PROTEIN IYROSINE PHOSPHATE.
           KLAGES S., ADAM D., CLASS K., FARGNOLI J., BOLEN J.B., PENHALLOW P.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SH3 DOMAIN; PHOSPHOPYLATION; ALTERNATIVE SPLICING
                                                                       91:2597-2601(1994).
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PROSITE: PROUDO; PROTEIN_KINASE_AIP: 1.
PROSITE: PSOOLOG; PROTEIN_KINASE_IYR: 1.
PROSITE: PSSOOLOG; PROTEIN_KINASE_DOM: 1.
PPOSITE: PSSOOLOG: SH2: 1.
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                                                                       C. NAIL, ACAD, SCI, U.S.A
                                                                                                    [2]
SEQUENCE FROM N.A.
STRAIN-BALB/C: TISSUE-THYMUS;
MEDLINE: 94255451
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Best Local Similarity 29.7%;
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                  SECUTENCE OF 41-505 FROM N.A
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505 AA;
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TPANSFEPASE; TYPOS
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* ** ** N. TRIBSSK - S ** UWSECVILLMEVEST SHAR FERMSEK FVSPAVE - KGYEKEPBBBBBBWH 452
                                                                                                                                         -64 ROHITTNERSALMWSEAVILMELVIRE-VPFACLSNMELSMKVALEGLEPTIPPGISPHVC 422
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TEANSEBEASEL ALTERINDING SER DOMAIN, SER DOMAIN,
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PROTEIN KINASE.
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BY SIMILARITY).
PROSPHORYLATION (AUTO-) (BY SIMILARITY).
28F5442A CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * '6. APTLEAGUMETERITETAT - LTAVVSE-EP-TYIVTEFFTF 98111 ALE 1811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIVE MARKET PROPERTIES TO THE TERANDEL TO THE TOTAL TO TH
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F. PATAL CHARGE CHEMINARY CH
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VIPITADE SKEPNA ENVELOPED VIRUSES: POSITIVE-STRAND: RETROVIRIDAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Postovenie Prograzja,
Miclingo Prograzja,
Postovenie Tomonie Ale Conoshima K., Hirayama V. Poshida K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NATTHE AND LOSE LOSE(1962).

C. CADAUNTIC ACTIVITY: AIP + A PHOTEIN TYRUSINE + ADP -
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Pred. No. 4.69e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ** TYEMS TP_OPESCHEELMKLTWKKDFTBERTFEVIGSFLE 517
                                                                                                                                                                                                                                                                                                   453 ILMGSOWEAEPARRPPERKIVEKLGR 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 - KIMKITHNITI AKREKETMIVETIEK 448
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PROSITE: PS00107; PROTEIN_KINASE_AIP; ; ; PROSITE: PS00109; PROTEIN_KINASE_TYP; ; ; PROSITE: PS00109; PROTEIN_KINASE_TYP; ; ; PROSITE: PS00790; PROPEIN_KINASE_DOM: 1; PROSITE: PS00791; RECEPTOR_TYP_KIN_V ]; ; PROSITE: PS01186; EGE_2; UNKNOWN_1. TRANSFERSE; TYROSINE-PROTEIN KINASE; ATP-HINDING; PHOSPHPHEN: RECEPTOR; TRANSFERSE; TYROSINE-PROTEIN, SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A PAMILY, HINLS I
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BY SIMILARITY.
PHOSPHORYIATION (AUTO-Y ON SIGNERATO).
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                                                                                                                                                                                                                                                                                                PUMAPYCIA, METAZGA, CHORDATA, VERTEBBATA: TELBARGIA: MOMMALLA
PUTHERIA: PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIANE: 92147681.

BOYD A.W. WARD L.D. MICKS T P. SIMPSAN N.3., SALVANIS F., WELCH K., LOUDOVARIS M., ROCKMAN S., BUSMANIS I.,

3. BIOL CHEW 267 3262-3267(1992).
                                                                                                                               01-DEC-1992 (REL. 24, CREATED)
01-DEC-1992 (REL. 24, LAST SEQUENCE UPLATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION SPINATE)
EPHRAIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (SPEPHA3 OR ETKI OR ETK OF HEK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: ATP - A PROTEIN TYROSINE = ADF .
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406 LEGLRPTIPPGISPHVCKLMKICMNEDPAKRPKFDMIVPTLE 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECHENTE OF 21-29 AND 840-860, AND CHARATERIZALITM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tryle
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                                                                                                                                                                                                                                                                                                                                                                                                 WICKS T.P. WILKINSON D., SALVARIS E., PCYS ALW. PROC. NATL. ACAD. SCI. U.S.A. 89:1611-1615(1992)
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64: Mismatches
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Best Local Similarity 27.8%;
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Query Match
Best Local Similarity 28:2%: Pred. No. 1 97e-40;
Matches 72; Conservative 72; Mismatches 91, Indels 20; Gaps 16;
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                                                                                                                                                                                                                                                                       389 EVPRADISHMENDERNALEGIEFTIFFORESPHYCKIMKICMNEEPAKFFMIVFILEK 448
VALEBLEW STILL FERHISEAGINSQFERENITE LEGVUTPSFP-VMIVIEWENSS 706
                                                        11 INVENTANTANT METERSHERMENDERFIERERWI PVIOACESPRAPHENTITHEMMEYGS 276
                                                                                                                 107 LOSELRKHUAGIVIQ DVOKUR-GIASOKKULSOKO WYRRD-LAARKULINSKLVOYV 762
                                                                                                                                                                       277 INNVIH ESIMEVVIGEÇAVEEMIJAMARAMAFUHTIBPLIPRHALNSBSVMIDETMIARI 335
                                                                                                                                                                                                                             753 SDEGISKVLEDDPEAATT IRGKIFTRWISPEALAYRKETSASDVWSYGIVLWEVMSYG 821
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'KABY TAL METAZHAL CHPRINIALA, VERTEBRATAL TETRAPODA, MAMMALIA;
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Bost Local Similarity 32.3%, Pred. No. 3.390-683,
Matches 81; Conservative 66; Mismatches 93; Indexis 11; Cups

Transconding 18; Conservative 66; Mismatches 93; Indexis 11; Cups

Transconding 18; Conservative 66; Mismatches 93; Indexis 11; Cups

Transconding 18; Conservative 66; Mismatches 93; Indexis 11; Cups

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYCOPERSICON ESCULENTUM (TOMATO).
FORARYCTA: PLANTA. EMRPYOPHYTA: ANGIOSPERMAE: DIVETYLEPFONEAE.
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STRAIN-CV. ALLSA CRAIG;
LIN Z., HACKETT R.M., PAYTON S., GRIFFW'N D.;
SUBMITTEE: (MAR-1948) TO EMHL GENDANK, DOHJ DATA HANKS.
EMBE, AJUÚSJ7; E1296723;
PROTEIN KINSE.
                                                                                                                                                                                                                                                                                                                            01-AUG-1998 (TREMBLREL, 07, CREALED)
01-AUG-1998 (TREMBLREL, 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL, 07, LAST ANNOTATION (FLATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05. TAST SEQUENCE DITATE)
05. TAST ANNITATE NOTATE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           981 AA: 107175 MW: 002DB613 CRC32;
421 VOKLMKICMNFDPAKRPKFEMIVFTJFKMUDA 452
                                                    421 VCKLMKICMNEDPAKRPKFDMIVPILEKMGDK 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRITE RZ9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1998 (TREMBLEEL D. 165 TAST
01-JUN-1998 (TREMBLEEL DK, 1AST
PHY-THETICAL 91.9 KD PROTEIN.
TYCOPERSICON ESCULENIUM (TOMART).
                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             946 AQLIVALIPLQ 956
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                                                                                                                                                                                                                   LT 3
065833
                                                                                                                                                                                                                                                                                             065833;
                                                                                                                                                                                                              RESULT
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                                                                                       6
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13.3%; Score 450; DB 10; Lengt 9 v. v.

Query Match

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380 FIQLMQSLKRLQ 391
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                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Best Decal Similarity 20:8% From No. 2.39e-64;
Matches 81, Conservative 74; Mismatches 96; Indels 19; Gaps 18;
                                 00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    359 EALLMEREETHERSADWASFAVLLWEIVTRBVPPARISHMEISMKVALRGIPPTIPPGIS 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8D DIEGI FIONREASEANSEINFOIVFOPAVAVPAVPITPIHKBETPAKIBGGEFSFVALIS 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14. RLE-HPALVAELMACKKEEV-YO-ILIETMSQOMLEMYLNKKEPYSLSIETVLELAFRE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 BILEBERGER VELDATES BARBETI CHRARFYSEVAVERBOINEVVELSORVERALDAR PAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 KAMENTHS VOVINKE LIKSMULLINDEMANZVALFOTSOTETCORERIOWATTPRMAR DSS
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                                                                                                                                                                                                                      727 TARAKARI LURIKALASIMALVORRITVYIN TUSEEKANTELSSYTAAGIDDWAAPDVI 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * 1981 CORRESPONDENCE NOT THE CONTRACT SHART SANCALES CERTIFICATION 421
                                                                                          550 IPWADLIDMEKIGASEPITVHENTWHUSCVAVETIMEOFEHAEFIKEELFEVAIMKELBH 609
                                                                                                                                                                                                                                                                                                                                                                                                                 307 FIHILEPLIFKHALNSKSVHIDSOMISKI-SKALVKF---SEQOPSEMI-AFAKVARBAL 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 RDEP--SNEKS DVTSFGVILWELAILQQFWMKINPPQVIAAVGENPKRLDIPSDLNPQV 784
                                                                                                                               TAC HRETHIRGHERMATERMANANALMENDE AND THE SHELL HAS 1881 TO 1881 THE SHELL HAS A SHELL HAS 
Best Local Simination crist. First N. 1 (98-106)
Matches 80: Conservative 77, Mismatches 97; Indels 11, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECURICE FROM N.A.
SHINN P., BURHLER E., DEWAR K., FENG T., KIM C., LI Y., SUN H.,
JOHNNY A., CORNAY A., MITTE D., OTH C., SHEN Y.K., TORIDMI M.,
VISOTERALA V., VI G., DAVIS R.W., FEDERSPIEL N.A., THEOLOGIS A.,
ECKER J.R.,
SUBMITTED (JAM 1998) 10 EMBL/TENBANK/DUBI DAIA BANKS.
BRBL. ACCOLLED (JAM 41.51.5K) 41.21.5K, 41.21.5K, 41.21.5K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARABIDOPSIS THALLANA (MOUSE-EAR CHESS).
EURARROLA, PLATIA, PRPHYTHRIA: ANTHUSEERMAE DICCIVIEDONDAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LASI SEQUENCE UPDATE)
LASI ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               419 PHUCKINKICKNETERFERFORMINFILERMOD 451
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01-00N-1998 (IREMBLRE).
01-AUG-1998 (IREMBLRE).
E2101-12.
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Dapparales, cruciferae.
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746 IPWNDLVIAERIGLGSYGEVYHADWHGTEVAVKKFLDQDFSGAALAEFRSEVRIMRRLRH 8°°
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 SVMIDEDWIARI---SMADVKE-SFACPSKMY-AFAWVAFEALGKKFEDTHFFGALAWSF 37*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S79 AVLIMELVINDVPFRADLSNMEISMKVALESIFFIIIFGISFFVOYINY 1000EDFFYRRY 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 GEVYRAEWNGIEVAVKKELDQDFSGDALIQFKSEIEIMLRL·RHPNVVLFMGAVIRPPN- 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
12.7%; Score 430; DE 10; Length 406;
Best Local Similarity 31.0%; Fred. No. 4.24e-62;
Matches 78; Conservative 65; Mismatches 96; Indels 13: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  205 GELWKGRWQGNDIVVKVLKVRDWSTPKSRDFNEECP-RIRIFSHPNVLPVLGAC_STREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 NLLVDKNWVVKVCDFGLSRMKHHIYLSSKSIAGIFEWNAFEVLANEFARFEKFURTUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         806 PNVVEFLGAV-IRP-PNLSIVIEFLFRSLYRILHPPKSHI-DEPFFFYMALDVAMOUV
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SHINN P. BUEHLER E., DEWAR K., FENG J., KIM C., LI Y., SUN B.,
SCHNN P., BUEHLER E., DEWAR K., CLI SHLK Y. Y. STIMI M.,
VSCTSKAIA V., YU G., DAVIS E.W., FEDERSPIEL N.A., THEOLOGIS A.,
ECKEF J.R.,
SUFMITTED (APP-1948) TO BMBL/JENRANK/LDBJ DATA BANKS.
EMBL, AC003981; G3063459; --
SPRQUENCE 1015 AA: 113014 MW, EB64F4FA CRC22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 PNVLPVLGACQSPPAPHPTLITHWMPYGSLYNVLHEGINFVVDQSQAVKFALIMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AFRETTOPSIS THALLANA (MOUSE-EAR CRESS).
EUKARYOTA: PLANTA; EMBRYOPHYIA; ANGIOSPERMAE; LICOITLEDONEAE:
CAPPARALES; CRUCIFERAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . Match 12.6%; Score 4.27; Db 10; Length 1015; Local Similarity 29.9%; Pred. No. 1.80e-51; as 79; Conservative 70; Mismatches 164; Indels 11:
01-JAN-1999 (TPEMBLPEL 05, LAST SEOURNCE UPDAIE)
01-JUN-1998 (TPEMBLPEL, 06, LASI ANNOTATION UPDAIE)
MAPRIC DELIAL-I PROTEIN KINASE (FRAGMENT).
APABITOPSIS THALLANA (MOUSE-EAR CRESS).
EURAPYOTA; PLANTA; EMBRYOPHYIA; ANGIOSFERMAE, DICCITLEL HEALT CAPPAPALES; CPUCIFERAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 HPTLITHWMPYGSLYNVLHEGINFVVDQSQAVKFALDMARSMAFLHILEPLTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 FSIL-TEFLPRGSLYPLLHP-PNHQLDEKPPMPMALDVAKGMNYLHISHFTVV;;
                                                                                                                                                                                                                                                                                                STRAIN-COLUMBIA;
HAMAL A. LEPRINCE A.S., JOUANNIC S., KREIS M., HENRY Y.:
SUBMITTED JUL-1997) IO EMBL/GENBANK/LL6J LATA BANKS.
EMBL, Y14199; E328681; -.
PPOSITE; PSO0108; PROTEIN_KINASE_ST: 1.
NOW TED
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01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 406 AA; 45965 MW; 90EF08EC CRC32:
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ory Maich.
15.4%: Score 352: DB 5: Length 422:
ost Loral Similarity 29.1%: Prod. No. 5.73e-46;
titles 78: Conservation 62: Hishatches i.3; Indels 15: Gaps 14;
44.2 THISTOTIVHROLKIDNLLVEHHWHVKVODFGLSRLKHNIFLSSKSIAGIPEKHAPEVLP 42.5
                                                                                                                                                                                                                                                                                                                                     123 NEET-SMERCHINVSCOVILMETALERENWRONNERLVVOANGFONKRLEIPKELDPVVG 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 TREPHEVATVERVEADSFANVELGIWNGVKVAIKILK-NE-SISNDEKFIKEVSSLIKSHH 193
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- 3.844.

- 1.0. (TREMBLREL. 01, CREATED)

- N.V.1546 (TREMBLREL. 02, LAST SEQUENCE UPDATE)

- N.V.1546 (TREMBLREL. 07, LAST SEQUENCE UPDATE)

- O1.405-1994 (TREMBLREL. 07, LAST ANNOTATION OPDATE)

- D1.107 STELLIN O180-10FFW (SIME NCL)

- D1.107 STELLIN O180-10FFW (SIME NCL)
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STRAILER (ANG-1993) TO PRRICIDERRANGE K. DAIN BARKS.
BURG. Tolores Graya45;
N. M. Derrorder Pkinase.
SHINE AZZ AA: 48243 MW; 14187339 CRO32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98" RIILEOWOTDPNERPSFAQLIEVL 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        **4 LIKUWASIPSCEPSETELLELEIMKSK 391
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SECTENCE PR. M. N. A. SIBAIN-AX-2; ACCEP PRISTIN.

PRI: 1338 AA.

PRELIMINARY,

MESCH.

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140 VAVKIMKLDNESQREIBEFLSBAACMKDFNHPNVIRGIGVOTPUSSGGIPRIMVILIGIAR 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 YGDLHTELLYSRLNTGPKYIHLOTL-LKFMMDIAWGMEYLSNEN-FURDO GAAFNORGE 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 YG---S--LYNVLHEGTNFVVDQSOAVKFALDMARGMAFLHTLERLIFFRALLNSFSVMII ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  329 EDMTARIS-MA-DVK-PS--FOCPGRMY-APA-WVAPFALORKPERTHREGALDRWSFAVI. 3-1
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                                                                                                                                                                                          188 IDFKOLNFLTKLNENHSGELWKGRWOGNDIVVKVLKVKDWSTPKSPIENHETPELATE
                                                                                        Match 10.2%. Some 446; DB 5; length 1448; Local Similarity 28.7%, Prod. No. 9.546-45; Conservative 64; Mismatches 114; Indels 14;
                                                                                                                                                                                                                                                          248 PNVLPVLGACOSPPAPHPTLITHWMPYGSLYNVLHEGINFVVHGGAVAVETALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.9%: SCOID 444; DB 11; Lugarl, Cll;
30.7%: Pred. No. 4.114-42;
ative 62: Mismatches 89; Indels 24;
                                                                                                                                                                                                                          1110 PNVVIEMGA-KI--DP-PCIFTEYLOGGSLYDVIHI-QKIKLNFORRYRHH
                                                                                                                                                                                                                                                                                                                                                                                              365 PEDTÜRRSADMWSFAVLLWELVTREVOPADLISNMEDGIRKVALEGIFFFFFFFFF
                                                                                                                                                                                                                                                                                                                          308 LHTLEPLIPRHALNSRSVMIDEDMTARIS - MA-TOVRENEGOTO-STRANKERENE
                                                                                                                                                                                                                                                                                                                                                              1221 GLUYNEK-VDUVSFGLUVYEIYTGKIPFEGLEGTASAAKAAFENTHFATHT
                                                                                                                                                                                                                                                                                            1165 LHSIQ-MLHRD-LTSKNILLDEFKNIKJADFGLATTLSDDMFFGGGT PROBJ.
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SCEMITTED (TUT-1996) TO EXEL TRIBLER TOBY TAIL BANKS.
EXEL. 004830, G1468983, -
PPAR: F00065, pkinase.
SECUENCE 1338 AA. 149926 Met. (KIETT-ELTECTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CD-1: IISSUE-TESTIS;
DOWDS C.A., BURKS D.J., SALING P.M.:
SUBMITTED (JAN-1906) TO EMBL. GENRARE, INSTEED STA BARKS.
PEMBL. LILE-25; GILGLIS;
PFAM: PF00069; pkinase.
TYROSINE-PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LT 10
062194
062194
062194
01-204
01-204-1996 (TREMBLREL 01, CREATED)
01-304-1996 (TREMBLREL 01, LAST SEGGEN E UPDATE)
01-204-1998 (TREMBLREL 01, LAST SEGGEN E UPDATE)
RECEPTOR PROTEIN TROSINE KINASE (FRAGMENT).
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Back Docal Similarity 20.7%, Pred. No. 4.11e-42;
Matchia 77, Consequentine CD, Mismatches 89; Indels 23; Saps 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         671 YOULGIELLISKLAIOWYINETIL TRIMATIACOMBYLSAPN. FLUFD . LAAPNOMLP 727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 (3) SHIENVERLOTHENVERLOTHEN STEEL STEEL TO SEE THE TO SEE THE SERVED SEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LINE, 90505000.
NAME OFFICE BOWMAN SIWIL DAMBON TILL, STANFORD WILL, EARP HIS.,
                                                                                       PRT: 994 AA.
0608055
01-WIT-1995 (TREMELEEL OF PREATER)
01-WIT-1996 (TREMELEEL OF PREATER)
01-WIT-1996 (TREMELEEL OF PREATER)
01-WIT-1996 (TREMELEEL OF PAST SECTION UPDATE)
0-WIT-1996 (TREMELEEL OF PAST SECTION UPDATE)
0-WIT-1996 (TREMELEEL OF PAST SECTION)
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Home saelens (Homen).
Porrapyla: Metalus. Chimeria. Vemiebrata. Thiparoda. Magalla.
Eutheria: Primates.
                                                                                                                                                                                                                                                                                                                                                                 CHOPDATA, VEPTEBPATA, TETPAPODA, MAMMALIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 FOTENTIAL.
391 CHEN TYROSINE KINASE PROPPTOR.
110156 HW. SCEP4291 DRG32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN 56, TISSUE SPIZER;
SNOOGRASS H.R.;
SUBMILLED (FILE) (FILE) (TENT), STREAMF, LIET CAIR BANKS.
BNBL: 021301; G889970; -...
PFRM: PF00041; fas.
PFRM: PF00041; fas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00059; pkinase.
                                                                                                                                                                                                                                                                                                                                       MIS MUSCULUS (MOUSE).
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334 AA.
   441 MIVPILENMOD 453
                                                                                                                                                                                                                                                                                                                                                                        ECKARYOTA: METAZOA:
EUTHERIA: RODENTIA.
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                                                                                                 RESULT
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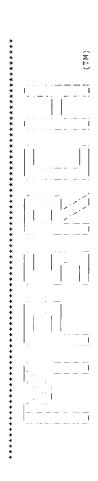
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Ω Ω 17 S

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183 AVKKVRDIKETDIKHIRKIKHPNIITFKGVGTQAPG-YGTIM-BFGAQGQLYEVLRAGRF 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 AVKKVPDLKEIDIKHLRKLKHPNIITFKGVOIQAPO-YGILM-EFGAGGGLYEVLRAGRP 2007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264 KSTKWSFAGIVAWWAPEVIPNEPV-SEK--VDIWSFGVVLWELLIGEIPVKDVDSSAIIW 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::| ||::| ::| ||::| | ::| | ::| | ::| | ::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 -VT-PSILVDWSMGIAGGMNYLH-LHKIIHPD-LKSPNMLIIYDDVVKISDFGISKELSD 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chery Match
Best Local Similarity 32.3%; Pred. No. 1.04e-41:
Matches 73; Conservative 56; Mismatches 81; Indels 16: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 -VT-PSLLVEWSMGIAGGMNYLH-LHKIIHPD-LKSPNMLITYDRVVYISTFTISKELSK
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01-NOV-1996 (TPEMBLPEL) 01, LASI SEQUENTE HEDATE)
01-UTN-1998 (TPEMBLEEL) 05, LASI MUNCAKION UPDATE)
ZIPPER (LEUGINE) PROTEIN KINASE (SEPINE, HELMINE ERLIELK MIJANE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 FVVDQSQAVKFALDMARGMAFLHTLEPLIPPHALNSRSVMIDEDMTARIS-MANNES
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9.8%; Score 331; DR 11: 1ength 888;
Best Focal Similarity 32,3%; Fred. No. 1.04e-41;
Matches 73; Conservative 56; Mismatches 81; Indels 16:
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EUKARYOTA: METAROA: CHOPDATA: VEPTEBRATA: TETRAPODA. MAUMATTA:
EUTHEPIA: PODENTIA.
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SEQUENCE FPOM N.A.
MEDLINE: 94311945.
PEDDY U.R., PLEASURE D.;
BACCHEM, BACHEM, BACHEM, 100 612-620(1994).
BERN: 107359, G561543.
PFAM: PF00069: pkinase.
SERINE/THRENNINE-PROTEIN KINASE.
RSG AA: 92188 WW. 07331597 CF032.
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STRAIN=CD-1: TISSUE-BRAIN;
MEDLINE; 9507410.7
HOLZMAN L.B., MERRIT S.E., FAN G.;
HOLZMAN L.B., MERRIT S.E., FAN G.;
J. BICL. CHEM. 269:30908-30817(1994).
EMBL; U1436; G602678: --
MOT: NOT-102689; DER.
PFAM. PFONOE); DER.
SEQUENCE 888 AA; 96083 MW; 4E966E5E CRC32;
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Marth
Orth Similatity (2.3%) Fred. No. 1.66-41; Length 888)
st 73; Couservation 56; Mixmatches 81; Indels 16; Gaps 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marks.
Thi Similatity 28.0%: Prod. No. 2.646-41;
S. Tai Conservative 63: Mismarches 198: Index: 1:: Saps 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.8 AVKKVRDIKTITTKHIBEIKHPHIIIFKGVOIQAPO-YOILM-BFGAUGGIYEVIRAGRP 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DER.
WYS MYSTIDS (MODSE).
FITARE IN METAZON: CHORDAIN VERTERRAIN: THTRAPODA: MAMMALLA:
FITHERIA: RODENTIA.
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                                                     Tober:
| PERP | 1497 (IMPERISED: D2. TREATED)
| FERM | 1297 (IMPERISED: D2. TAST SECTENCE TROATE)
| FERM | 1498 (TREATERED: D6. LAST ANAMORALE HIPDATE)
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FEB-19-7 (TREMELEEL 12, LAST SEQUENCE UPDATE)
FEB-19-19-4 (TREMELEEL 16, LAST ANNOTATION UPDATE)
SHOT.
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SIBATN TANTIN S.
AMDILINIA "ASSMALL"
MAKABARI F. BUND'S. KOLIMA I.. SALGY K.I.
HINES DEV. [CLICAG-LEGG(1996).
HINES DEV. [CLICAG-LEGG(19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TEST THILD MELAN-MASTER (FRUIT FLY).
HTKARY (A) MELAZO'A: ARTHROPODA; INSECTA: DIFTERA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       000671 Pkingso.
888 AA: 95957 MW: 806A0E87 CRG32;
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PRELIMINARY;
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Computer modelling design of specific affectors - using three-dimensional conformation of enzyme-affectors - using three-dimensional conformation of enzyme-affectors - using three-dimensional conformation of enzyme-affectors - using the inventors provide a crystal structure of cAMF-dynadom; in the inventors provide a crystal structure of cAMF-dynadom; in index the consensus feature common to all peptide existing is inhibitors of cAPK. In addition if confains other leafures the consensus feature common to all peptides existing convey unique high affinity binding characteristics, from an analysis of FNI(5-24) a template is derived from which all other convey unique high affinity binding characteristics, from an interest of the KNI(5-24) a template defined by a number of linear convey than seen to modelled and from which other inhibits contact with PNI(5-24) in a complex, evaluating the protien complex, examining the amino arise of the the protien complex, examining the amino arise of the first protein kinase correspondent contact for an inhibitor of the first protein kinase. In the cashing the contact for an inhibitor of the first protein kinase. In the cashing the contact of the first protein kinase in the cashing the contact of the sic protein kinase correspondent bomology to design an inhibitor to protein complex of the sic protein kinase this methodology to design an uniform time cashing the protein contact of the sic protein kinase correspondent bomology to design an uniform time cashing the protein contact in unknown the contact of the contact of the contact of the contact of the contact for an uniformation of the contact of the contact for an uniformation of the contact for an uniformatic for an u
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Inhibitor peptide; cellular protein kinase; profoconvanges;
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These residues are incorporated into the appropriate position.
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87,4%; Pred, No. 2.710-155;
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22-JUL-1991, US-735614,
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the sequence outsists of the N-torminal amino acids of the beta-
aalactesidase gene fused with the lok gone. It is produced by
E-coll translotmed with a recompanion vector (see $1592), It is
useful for producing an articoly specifically immunoracitive with
only a low purchase full principality is possible to the with
recognise is your derived polypeptides in human cells.
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                                                                           1. 4
14.20.1 standard: Protein: 417 AA.
R1420.1
13-DEC-1991 (first entry)
(bell galantidias, Noternin:); (ith game prof fusion protein.
Multi-choling site.
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Bast Local Similarity (6.9%) Prod. No. 9.766-113;
Matches 171, Conservative 39, Mismatches 45, Indels F
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R85929;
R85929;
R4 FEB-1996 (first entry)
Protein tylosine Kinase LpTK2.
Follo: Gillerentiation.
                                                                                                                                                                               /note- "beta galactosidase fragment"
27..417
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28-DEC-1989: UP-338268.
(TOFT ) TOFTYAMA SODA KK
             241 erptfeylgafle 253
                                    244 ERPIFEYIOSFLE 256
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Agonist antibodies which activate specific protein tyrosine kinase(s) - also activate chimeric proteins of kinase extracellular domain and ig constant domain, useful for studying, and therapectic modulation of, cell growth and ifferentiation bisclosure, Page 56-58; 125pp; English.

DNA probes based on protein tyrosine-kinase (pTK) sequences were used to screen cDNA libraries to identify movel [PTK] general Residence of the interpretation of megakarycoptic cell libraries. The encoded novel pTK, LpTK2 (R855029), shows homology to known pTKs, and can be used to design drugs that modulate pTK.
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Bost Local Similarity 54.2%; Fred. No. 6.2%-90;
Matches 141; Conservative 56; Mismatches 59; Indels 4: Gaps
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FIK, protein tyrosine kinase; catalytic domain; c-bit; necus
lymphocyte; amplification; primor; polymerase chain reaction
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                                                                      Tsai SP;
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22-JAN-1993, U00586.
22-JAN-1992; US-826935.
(NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
Arraham H, Cowley S, Groopman J, Scadden D:
N-PSDB; Q49754.
                                                                      Matthews W,
                                                                          Lee JM,
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04.AFR.1994; US.222616.
(GEIH ) GENENTECH INC.
Bennett BD, Goeddel D,
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227 linnsiglikriasagianuwediwnotipvavkrikpgsmdpndfirsagimknirhpk 288
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                                                                                                                                                                                              Score 1974: DB 8: Length 505;
Pred No. 6.35c-90;
56: Mismatches 59: Indris 4: Gaps
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A brk (brown runer than ) committee as a committee of the runer call line 1.47b, 2
NAA king my propared from himan broast timon cell line 1.47b, 2
NAAs kore is lared. The slightly longer close lambda 12 (Jalies)
winder its (fisher) which was identified as a nore) putative interverse kinds of use as a produced in the broast
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Stated is alven in the specification, however is missing from
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Broas' 'umor kinase, byk]
Preas' 'umor kinase, lik; profefe-Tyrogloc-Kinase, Fik;
Livas' 'umory metastasis; prognosis; diaduosis, F-475.
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                                                                                                                                                                                                                          Cornel Similarity 54,28, ors (4): Conservative
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                                              The problems on the
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The amino acid sequence is represented as found in the specification.
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                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                Score 1033; 58-12; Lendth 45; Pred. No. 5.896-86;
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R15156;
12-FEB-1992 (first entry)
Abelson Related Gene, A transcript.
Ātg. diagnosis; therapy: tumour: abl protoconcounce.
                                                                                                                                                                                                                                                                                                                            53; Mismatches 60;
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22-OCT-1991, 554029,
30-JUL-1990, US-559029,
(USSH ) NAT INST OF HEALTH.
KIUD 6, AFRONSON SA, KING CR;
WPI: 91-353425/48
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Best Local Similarity 53.4%;
Matches 133; Conservative
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les 130; Conservative
tumor metastasis.
Sequence 451 AA;
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198 gilliblytkiski ig Javaskylilve Jveap PPT TRESLætakfokkuppeert 247
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 Amutant IR is claimed which may have a mutated alpha-chain, esp. at the mutant IR is claimed which may have a mutated alpha-chain, esp. at the precursor processing size. The beta-chain may be mintated, e.g. by deletion of the transferences of the transferences with may be inactificated. Fig. 5 is a comparison of project and human EGE receptor sequences with that of HIR in the cytoplasmic sequence. 254 Am.
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(SDIM) GENERAL INC.
Rell UE, GILLOU A. Bammachandran J.
Will BE LESSE(35).
New DNA choulding lusualla receptor or its fragments - used for
synthesis of receptor and mutants for thorsapeutic and itsgnostic
                                                                                                                                                                                                                                                                                                                                                                                                                  18.5%, Socke 942, DB 3, Length D54; Best Local Similarity 50.5%, fred. No. 3.550-77; Marches 140, Construction 39, Mismitches 51, India 8,
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R94538:
10-707-1998
Droughlia stoled tyrosine Kinase.
Proteinsmite tyrosine Kinase. 2000. Lucnatogoletic pell:
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65...155
/label_SH2_domain
186..425
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Sequence of consider areas
Therapy diagnosis, insuling
DF 1923/2-8.
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                                       489 spadrpsfaethqaf 503
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10-FEB-1985; 300894.
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Disclosure, Fig 5D; 40pp; English.

The human gene encoding this protein is closely related to but distinct from the abl proteince and is a member of the tyrosine tinner from the abl proteince and is a member of the tyrosine by analogy with crabl, the alternative 5' arg sequences have been designated A (1014985) and B and it is assumed that they are joined the the arg second exon.

The amino acid sequence is represented as found in the specifical
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Stimulate and 28-29. dopp. English.

The amine acid sequence (P945:8) of Proceedilla sto280 tyrosine kinase was compared with the sequences of 2 members of a respect tyrosine kinase family. PHY (R945:4) if (F445:5) and TEC (F445:5), and and decided and teceptain forms of the compared with novel homen cytoplasmic tyrosine kinase BMX (see also P9453). Close hemology was found.
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Best Local Similarity 48.6%; Pred. No. 2.68e-76;
Matches 119; Conservative 54; Mismatches 70; Indels .
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Akelson Pelated Gene, B transcript.
Arg; diagnosis; therapy; tumour; abl proto-oncogene.
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/label= Tyrosine-kinase_domain
                                               187. 209 // /label = ATP-binding_region
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R15157 standard: Protein; 1182 AA.
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30-010-1990, US-559029.

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Alizals K.

Willias K.

Willias C. Frack/2],

Willias C. Bornardon Kinasc BMX and related DNA - useful to be simple tyrosine kinasc Followshi.

You have the following the finasc FD (5945%) is expressed in mixing a newly identified non-receptor tyrosine of THO and 2 other neutors of a newly identified non-receptor tyrosine kinasc found. Tr (845%) is expressed in mixing a newly fidentified non-receptor tyrosine vinasc found.

Will bik (845%), when compared Will that of newel cytopassine tyrosine kinasc found.

Suppoper A. Singal MA.

Suppoper A. A.

Close homelony was found.
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                                                                                                                                                                                                                                                                                                             * PESTRIBURY GOGS GEVERNGTWNG-TIKVA!KTIMPGTOMPDAFÜGNAGIMKKIRHDKL GI
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                                                                                                Score 919; DB 3; Length 1182;
Pred. No. 7.476-75;
52; Mismatches 74; Indeis 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label: N-terminal_region /label: N-terminal_region contails the plecks: Tin homology region consisting 18 4 - 234 | 184...234 | 184...234 | 184...234 | 184...234 | 184...234 | 184...234 | 188...40main
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Fig. 1 Major. Similarity 47 78 Prod. No. 1 474-59.

Mit. Los 1.41 Fig. 54 78 Fig. Mismarches 73. Indois 2
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                                                                                   (%) Similarity do.4%;
126; Consommer
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Section of
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                                                                                                                                        554 mwelftegrmpfekntnyevvtmytrahrlhrpklatbylmmml; wqmqmuqsfort.
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191 LTELVIKGRVPYPGMVNREVLEOVERGYRMPCPGGCOPESCHELLER († 1911)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoplasmic tyrosine kinase BMX and related DNA - 18401...
Stimulate haematopolatic cell growth.
Disclosure: page 21-23; 40pp; English.
Cytoplasmic tyrosine kinase BTK (R94534) is setter integrated tyrosine kinase BTK (R94534)...
The surrented rytosine kinase BTK (R94534) is setter integrated tyrosine kinase and 2 orber members of a newly-identified non-receptor tyrosine kinase tamily. ITK (R94535) and TEC (R94534), and of the bracephila Sto28C tyrosine kinase (R94534), worn compared with that of nevel cytoplasmic tyrosine kinase HMX (see also K44544).
Sequence 659 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytoplasmic tyrosine kinase; BMX; haematopoietic cell; cell growth; cell proliferation; tumour; diagnosis; the approximate
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Bost Local Similarity 41.2%: Pred. No. 4.4 Pred. No. 8.4 Pre
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/note- "the N-terminal region roundins
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R94534 «tandard: Protein, 659 AA.
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WPI; 96-209
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12: THE CLASS OF VOTES OF A STANDARD SETTING THE STANDARD SANDERS OF STANDARD SANDARD SETTING SETTING SETTING SANDARD 
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Best bocal Similarity 40.5%, Fred. No. 1.28e-65,
Materies 104, Conservative 71, Mismatches 78, Indels 4: Gaps
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218.1263.263
7.1386. 5882.40main
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/cote "sec homology domain II"
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24-050-1992: 05-985998.
21-FEB-1995: US-391615.
(REGC ) UNIV CALIFORNIA.
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WPI: 98-401601,40.
N-PSDB: T45648.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The New Jordon Annae BMX and related DNA - useful to stimulate haematopoietic cell growth.

The Cytopiasmic tyrosine kinase BMX (P9453) is capable to stimulate haematopoietic cell growth.

Stimulating growth and/or proliferation of haematopulotic relation growth and/or proliferation of haematopulotic relation to the product of a cDNA clone isolated from a human time to the latest product of a cDNA clone isolated from a human time to the latest of a cDNA clone isolated from a human time to the latest for call transfer for call transfer kinase (R94538). It is useful as a marker for call transfer kinase (R94538). It is useful as a marker for call formation and differentiation and for various types of tumour formation and in the diagnosis and treatment of diseases resulting from deregulated tyrosine phosphorylation.
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10-JUL-1996 (first entry)
BMX tyrosine kinase
Cytog lasmic jrr sine kinase, PMX, basmarrprictic cell)
Cytog lasmic jrr sine kinase, PMX, basmarrprictic cell)
Cell growth; cell proliferation, tumbur, liaguists, therapy.
Homo sapiens.
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of a 7-strand antiparallel beta-sheet
213..265
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/label= Tyrosine-kinase_domain
423..445
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/label= ATP-binding_region
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07-001-1994; US 320432.
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ALIGNMENTS

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NTRY	TVCHYS #type complete
	protein-tyrosine kinase (EC D.7.2.22) yes / chicken
_NAM	kinase-related transforming protein yes
ORGANISM	#formal_name Gallus gallus #common_name chicken action=1001 #ecations verteir 1000 miletime
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SNOIS	\$03324; \$05283; \$0168a
RENGE	503324
authors	Zheng, X.; Podell, S.; Sefton, B.M.; Kaplan, P.L.
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0.11.	The Sequence of chicken offes and follows).
#Cross-relerer #access-relerer	ICES MOID:891Z8ZU4 SGCCACA
OH##	type mBNA
##residues	1.541 ##label 2HE
	exences EMBL:X13207
PEFEFENCE	505283
#authors	
#submission	submitted to the EMBL Data Library, October 1988
#accession	S05283
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## millind_site myris[y]afed amino end (Gly) (in mature
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Similarity of its transforming dene profession to that of Rous
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Phosphotransiciase: transforming protein: tyrosine-specific
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Protein-tyrosine kinasa (EC 2.7.1.112) pres:
#formal_name Homo supjects #vommon_name man
31-Dec-1988 #sequence.revision 31.7eve(pake frex) and
*binding_site physphate (771) (covalent) (by autophosphorylation) *status predicted *length 528 *molecular-weight 59250 *checksum Ga
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autophosphorylation) #status post rec;
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                                   SUMMARY
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kinase_related transforming protein (yes)
#formal_name Xen_Fus laevis *profine_name African clawed ited
14-May-1993 #sequence_revision 14-May-1993 #text_change
08-Sep-1997
                                                                                                                                                                                                                                                                                           A45501 #tyrpe complete
protein-tyrosine kinase (EC 2 7 1 112) yes a African clawed
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121 VIHFBLRAANILVGENLVCKIADFGLAFLIEDNEYTAFQGAFFTFKTAFRAALYGRETI 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Steele, R.E.; Irwin, M.Y.; Knudsen, C.L.; Gollett, J. Fero, J.B.
Oncogene Res. (1989) 1:223-233
The yes proto-oncogene is procent in amphibians and contributes to the maternal RNA pool in the congression.
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#domain SH2 hardlogy #label SH2',
#domain protein *Knase hardlogy #label *TH3',
#region protein himsaw ATF *LL2', wolf *Thagth 527 #relegular-wolght #og91 #recksum 7604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Steele, P.E : Irwin, M.Y., Enddsen, C.L.: Collett.
Fero, J.B.
Submitted to the EMRL Pata library, February 1987
S08517
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Best Local Similarity 96.9%; Pred. No. 0.00e+00;
Matches 24%, Cinservative f, Mismotobes 2 Indels (
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##residues 1-250,'S',252-537 ##label ST2
##czcss-references EMBL:X14377; NTD:367272. FT
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Hannia, 3.; Stille, S.; Schartl, M. Oncogne (1991) 6:34-349
Conservation of Structure and expression of the cayes and iyn
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Profession prosing Kinase (EC 2.7.1.112) yes - Niphophorus
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24-Sep-1967 #sequence_revision 24-Sep-1967 #text_change
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Host Lord: Similarity 44.1%: Prod. No. 0.000-10;

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##FORTONSTROLOFORCOS EMBLIXS44732 NID:464493; PID:464484
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Anderson, S.K.; Gibbs, C.P.; Tanaka, A.: Kine, H.... I., Je
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Mol. Cell. Biol. (1990) 10:20+5-2040
Identification of a newel heuronal Chemotric expensions in
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J. Neurosci. Res. (1989) 24:89-96
Neuron-specific splicing of G.SKC MA in Lunde Heale.
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12. YTEFDLEARNILVSDNLVCKIARF STAFT FROMFYTAF, DAFFEL BETTALLAND VOOL.
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Activation of the Delialar art gene by transducing
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#cross-references MUID:87064539
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TOURSHOLD OF The Collidar SEC Gene and 37 adjacent symptoms in avian sarrows views PK2255.
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W. 1. John Seminarity 89.1%: Prod. No. 1 510-902.
87. 1038 - 274; 0.0860.001 0 17 March 20.2.
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Doral, T.; Levy, J.B.; Kana, L.; Briege, J.S.; Wane, J.B.;
Mol. Cell. Biol. (1991) 11:44:65-4174
Analysis of CDNAs of the professioner steri heteropeasing
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                                                                                                         #duthors Martinez, R.; Mathwy-Provot, B.; Mothards, A.; Balling, #journal Science (1987) 237:411-415

*title Neuronal pp60(c/src) contains a six-amine acid lisent; relative to its non-neuronal contropart.
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the authors translated the cobas AAT and TAX F.;
residues 301 and 525 as The and T.; prespectives.
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#fille An alternative non-tyrosine protein Minase project of the critise an alternative one in chicken skeletal muscle.
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#fiftle The two Manopus laevis SPC genes are to expressed a produces functional pp(60src).
#cross-references MulD:89278134
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01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PROTO-ONCOGENE TYPOSINE-PROTEIN FINASE VES (BC 2.7.11112) (PG) TES)
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PROSITE: PS00109; PPOTEIN_KINASE_IYR: 1.
PROSITE: PS50001; SH2; 1.
PROSITE: PS50001; SH3; 1.
PROSITE: PS50002; SH3; 1.
PPOTT-ONCOGENE: TYROSINE-PROTEIN KINASE; HPOSHDEPTIATION; TPANSEPARE: APPRINGS; MYELSTATE (MY SIKILAHIT); MAIN.
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TYROSINE KINASES IN THE CATALYTIC
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01-001-1993 (REL. 27. LAST 6 NATON UPDATE)
01-001-1996 (REL. 34. LAST 6 NATON UPDATE)
PROTO-ONGOGENE TYRCEINE PROT 1 KINASE YES (BC 2.7.1
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BUTHERIAN RODENTIA.
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THINKS ALTHOUGH THE SECURITY OF                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLAGES S. ADAM D. ELSEMAN
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PPOTEIN KINASE.
AIP (BY SIMILARITY).
AIF (BY SIMILARITY).
BY SIMILARITY (BY SIMILARITY).
PHOSPHOWILARITY (AUTO-) (BY SIMILARITY A 4455500 GNOSZ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      330 LVPLYAVVSEEPIYIVIEFNSKGSLIDPLKEGDGKYLKLPQLVDMAAGIALGIANIEERNN 989 (11911) | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
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                                                                                                                                                                                                                                                                                                                             270 IPPESURLEVKLGGGGFGEVWRGIWNSTIPVAIKILKESIMMELARLIENGIMMERNEY 329
ATP (BY SIMILARITY).

BY SIMILARITY.

PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

V > 1 (IN NEE- 2).

Wissing (IN NEE - 2).

Cleenes (NOLL).
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01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
01-JUL-1989 (REL. 13, LAST SEQUENCE UPDATE)
01-RYV-1995 (PEL. 32, LAST ANNOTATION UPDATE)
PROTU-UNCOGENE IXROSINE-PPOTEIN KINASE NES (EC 2.7.1 112) (P61-NES)
                                                                                                                                                                                                                                                                    i, Indels 0: Gaps
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                                                                                                                                                                                                                                                                                                                                                                         XENOPUS LAEVIS (AFRICAN CLAWED FROG)
EUKARYOTA; METAZOA; CHOPDATA; VERIEBRATA; IETRAPODA; AMPHIBAA;
                                                                                                                                                                                                            Query Match
Bust Loual Similarity 97.3%: Pred. No. 0.00e-00:
Matches 249; Conservative 5: Mismalothes 1. Indols (
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249
524 A1
2995 A1
390
420
60357 WW
                         303 303
394 394
424 424
372 372
374 390
541 AA; 60630 M
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61 LVPLYAVVSEEPIYIVTEFMTKGSLLDFLKEGEGKFLKLPQLVDMAAQJALKSMAVITEAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY, PHOSPHOREITATION (AUTS.) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                1 IPRESLRLEVKLGOGCFGEVMMGTWNGTTKVAIKTLKPGTMMPFAFTGEAGEMKREFHER
                                                       388 YIHRDLRAANILVGENLVCKIADFGLARLIFDNEYTARGGARFFFFFFFFFTALLAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11) Mismatches 4: todols 1: Ours
                                                                                             448 KSDVWSFGILQTELTTKGRVPYPGMVNREVLEGVERGYRMFGTGGTPESTHELMN.
                                                                                                                                                                                                            01-AUG-1992 (REL. 23, CREATED)
01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE YES (EC 2.7.1.112) (P.
                                                                  TABLE LONGON CAAS
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                                                                                                                                                                                                                                                                                                                                                                              71:14
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EUKAKYOTA: METAZOA: CHORDATA: VERTEBRATA: PIRCES;
OSTEICHTHYES: ACTINOPTERYGII: ATHERINIFORMES;
                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYPOSTME PROTEIN TYROSINE PHOSPHATE.
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                                                                                                                                                                                                       544 AA
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PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE: PSOO107: PROTEIN_KINASE_ATF; 1.
PROSITE: PSO0109: PROTEIN_KINASE_TYR; 1.
PROSITE; PSSO011: PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prod. No. 0.
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Conservative 11; Misman
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HANNIG G. OTILLE S., SCHARTI, M.;
ONCOUENE 6:361-369(1991)
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159 256 SH
274 531 PR
284 292 AT
306 306 AT
397 397 AT
397 397 PH
427 427 PH
                                                                                                                                   508 DPDERPIFEVIQSFLE 523
                                                                                                                                                      241 DPDERPTFEYIOSFLE 256
                                                                                                                                                                                                  STANDARD;
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MEDLINE; 91187435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS50001; SH2;
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P27447;
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BINDING
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333 LVPLYAVVSEEPIYIVTEFMGKGSLIDFLKREHRKLFOLVEMASOTTETTETTE

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Gaps

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Mismatches

SOME 1898; DB I; Length 5:0; PrN. No. 0.00e+00;

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A SAMPERILY STANDARD 
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                                                                                                                                                                                                                                                                              121 PIRKLISARILVSENIVORTALFORTEDENEVTARIORETIKMIANRALVORFIT 180
FILEFERENCE TELEFORM THE STATE FROM THE STATE OF THE STATE S
                                                                                                                                                                                                     393 YIHRDIRAMILVADNIVOKIARFELARLIRDNIYTARGGAKFPIKWIAPBAALYGRFII 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P12907-1989 (REE. 12, CPEANED)
01-007-1989 (REE. 32, LAST SECRENCE UPDATE)
01-NOV-1998 (REE. 32, LAST SECRENCE UPDATE)
15-001-1998 (FF: No. LAST ARROTATION UPDATE)
PROJECTOROUGHE TIRUSTHE-FRUTEIN TINASE SET (EC 2.7 1.112) (PEG-SPT)
(G-SRC).
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MIRK I., FACUESKY BLOW, FEEL M.F., PREFIGUES M., STERNBACH D D
CONSIER I.G.)
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BONO SAPIENS (HUMAN).
THEFT A METALIA THORDATA VEPTEBATA TETPAPODA: MAMMALIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-194 PPOM N A
MEDLINE: 97-257-201
TANÀRA A., SIRBA C.L., ARTHUR R.P., AMPERSON S.K., KUNG H.-7
FUJITA D.J.;
MCL. CELL, BIOL, 7:1978-1983(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEĞUERKOL OF 275-525 FPOM N A
MEDLINE, ÖJLƏJƏSI.
PARRER R.C., MARDON G., LEBÖ R.V., VARMOS H.E., BISHOP J.M.
M.L. JELL. BIOL. G.231-4-44(1955)
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NO 5 N . W. C. T. N. TAVIS D D . FINE N.C. WILLIAPD D.H. JP.
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AU W. AARRIN WELL FIRM T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E- E UNITA
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AKERNOLN J.K., LIEPY T. TANAKA A. MEL, CELL, BIOL, 5:1122-1129(1985).
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P12931:
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444 KSEVWSFGILLIELIIKGPVPPSAVVNEVLLLVEFGYFMFGFFEGFEGLHDLMGGGWPR 503
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Best Local Similarity 88.7%; Pred. No. 0.00e+00:
Matches 227; Conservative 18. Mismathles 11. Indels C: Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MARMY TOUGHT, PROTEIN_KINASE_AIP; 1.
PROSITE: PS00107; PROTEIN_KINASE_IYR: 1.
FROSITE: PS500109; PROTEIN_KINASE_DOM; 1.
PROSITE: PS50001; SH2: 1.
PROSITE: PS50002; SH3: 1.
IKANAFERAE: TYPOSINE-PPOTEIN KINASE; PROTO ONCOGENE: PHYSHE NY
AIP-BIXDING; MYRISIYLATION: SH3 COMAIN, SH2 COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHOPYLATION (AUTO-).
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20456525 CRC32;
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SNC_AVISI STANDARD, F
P14085:
01-JAN-1990 (REL. 13, CREATED)
EMBL: K03212; G3284460; JOINED.
EMBL: K03213; G388460; JOINED.
EMBL: K03214; G388460; JOINED.
EMBL: K03215; G388460; JOINED.
EMBL: K03215; G388460; JOINED.
EMBL: X02647; E303307; --
EMBL: X03995; E303307; --
EMBL: X03995; E303307; JOINED.
EMBL: X03996; E303307; JOINED.
EMBL: X03998; E303307; JOINED.
EMBL: X03998; E303307; JOINED.
EMBL: X03998; E303307; JOINED.
EMBL: X03998; E303307; JOINED.
EMBL: X03999; E303307; JOINED.
EMBL: X03999; E303307; JOINED.
EMBL: X03999; E303307; JOINED.
EMBL: X04000; E303307; JOINED.
PDB: IHCS: 15-SEP-95.
PDB: IHCS: 15-SEP-96.
PDB: IANT: 20-AUG-97.
PDB: IANT: 20-AUG-97.
PDB: IANT: 08-APR-98.
PDB: IANT: 08-APR-98.
PDB: IAIL: 08-APR-98.
PDB: IAIL: 08-APR-98.
PDB: IAIL: 08-APR-98.
PDB: IAIL: 08-APR-98.
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25 247 SH2
275 222 PPC
275 297 ATI
297 297 ATI
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298 388 419 PPC
525 AA, 59703 MW.
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| CAN-1 -- (RED. 14 LAST SEQUENCE OPDATE)
| N V-1 -- (RED. 24 LAST ANN-TATION UPDATE)
| YE SINE-PRITEIN KINASE TRANSFORMING PROTEIN SRC (EC 2.7.1.112) (P60-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·.
                                                                                                                                                                                                                                                                                                                                                      242 THEBSTRIEVKIANGSTESEVENGTWOGTTRVALKTIKPGTMSPEAFLGEAGVWFKIRHEK 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6. IVILYAVVSEEDIYIVTEFHIKGSLLDELKEGEGKERKEPOLVDMAAGIAGSHAYIEKHN 120
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                                                                                                                               V-SAC.
AVIAN SARCOMA VIRUS (STRAIN S2).
VIHITAEL SS-RNA ENVELOPED VIRUSES: POSITIVE-STRAND: RETROVIRIDAE:
N' VIETNARE.
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Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FECKER CONCOCENE PROBLEM ONCOCENE PROBEHORY, ONCOCENE PROBEHORY, ATTOM ATP-PINCHAMO, MYRISTYLA (1 N.
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ATP (BY SIMILARITY).
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Wal Similarity 40,78,
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MELLINES HT064539
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01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN SHC (FC 2.7.1.112) (1400
                                                                         SEQUENCE FROM N.A.
MEDLINE: 87064539.
IKANA S., HAGINO YAMAGISHI K., KAWAI S., YAHAMOTO T. TOYOSHIMA K.,
IKANA S., HAGINO YAMAGISHI K., KAWAI S., YAHAMOTO T. TOYOSHIMA K.,
ILE BIOL. 6'2426'2438(1966).
-I.- FUNTION: THE PHOSPHOPROTEIN, REQUIPED FOR HOTH THE INITIALION
AND THE MAINTENANCE OF NEOPHASTIC THANSFORMALION, IS A PROTEIN
KINASE THAI CATALYZES THE PHOSPHORYLATION OF TYPOSTINE BESTOCHES
                                    AVINE SARCOMA VIRUS (STRAIN BI),
VIRIDAE: SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND: WEIROVIKIDAE.
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                                                                                                                                                                                                                                                                                                                                                                                                                       92.7%; Score 1801; DB 1; Lenath (eq. 89.1%; Pred. No. 0.00e+00;
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ATP (BY SIMILARITY)
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P15054;
01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SECUENCE TRYATE)
01-APR-1997 (REL. 35, LAST ANYONA PROPERTY.
                                                                                                                                                                                                                                                                                                                            MYRISTATE.
                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 89.18;
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PROTEIN KINASE.

PROTEIN KINASE.

A.E (BY SIMILABILY).

BY SIMILABILY.

PHOSPHORYLATION (AUTO-) (BY SIMILARILY).
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333 TIBELLE HELLE HE
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INSCEINE CROIEIN RIMAGE JEANGEPRNAT FROTEIN SPO (ET 2 7 1.112) (250)
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Fred. No. 0.008-00.
17. Mitmorthes 11: Indels 0: Japs
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                                                                                                                                                                                           AVIAM SARIOMA VIMUS (STRAIN FRODET).
VIRIDAE, 88-KKA EMVZLOFED VIRMSFS, FUSTITVE-STRAND, FFIRMVIRTEAD,
OMOOVIRIMAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIGAS CASCIALLOSAMENT (L.1 ANDSCELME) LE CAGLO49.
HOLLAND ELEL LOWNEY E A , PETEMBER M S , MOFELLER W I , MOCGNUPIL.
PAVLOVSKY AL, PARA K.S., SHAHRIPOUR A., HUMBLEI C., SAWYER I.K.,
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PROSITE: PSOCIOT: PROTEIN_RINASE_ATP: 1.
PROSITE: PSOCIOT: SHOUTH RINASE_TH: 1.
PROSITE: PSOCIOT: PSOCIETIES.
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RRA : HEALINE H. BAININE T.V., SVURGEA T., NEHURA
NAROZ : BYNDITCH A.V., MATSULA B.A., CALOTHY G.,
VIROL. 63:481-492(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEMILLED (APR-1991) IC EMBL, TERRANE, TIET DATA BANKS
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Boot Local Similarity 89.19.
Ratchia List List.
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KARAKOZ I..
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269 IPSESTRIEVRIGGGSPSEVMASTWANTIFVALKITRISTASSEART DAAGAGGGGGG 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 PSEVWSFGILLIELVIKSFVPYPSMVNFFVI BJVFFSYPMFGPFGGGESLHEIMFLGWER (190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
--- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
--- SIMILARITY: TO OTHER PROTEIN-TYPISINE FINASES IN THE CATALITIED DOMAIN. BELLONGS TO THE SF2 SUBFAMITY
EMBL: M17031; G201057; ---
                                                                                                                                                                                                                                                                            (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 YTHPELPAANILVGENLVCKIADFSLAPIISENEYTARGSAKFRIKWTAREAALTGEL
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                                                                                                                                                                                                                                                                                                                                       MUS MUSCULUS (MOUSE).
BUTHEVIDA, MENTACOA, CHOPLATA, VFFIEBRAIA, IETFAFILA, MANMALLA.
BUTHEVIA: PODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
PHOSPHORYLATION (ACTO-) (BY SOME
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diery Match
Best Local Similarity 88.3%; Pred. No. 0.00e+00;
Matches 226; Conservative 18: Mismatches 12: Indeis
SEQUENCE FROM N.A.
MEDLINE: 87263406.
MARTHEZ P., MAPLEY-PPEVOT B., RERNARDS A., BALLIMORE D.:
SCIENCE 27-411-415(1987).
-!- CAIALYTIC ACTIVITY: ATP - A PROTEIN IYROSINE = ADP -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYRISTATE (SY STMTLARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE: PS50001; SH2; 1.
PROSITE: PS50002; SH3; 1
IFANSFERASE; IYPOSINE-PPOTEIN FIRESE; PROTINCENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATE-BINGING, MYRISTYLATION, SH? DOMAIN, SH2 DOMAIN. INII_MET 0 0 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN KINASE.
ATP (BY SIMILARITY).
AIF (BY SIMILARITY).
                                                                                                                                                                                                                 01-NOV-1988 (PEL. 09, CREATED)
01-NOV-1995 (REL. 32, LAST SECUENCE UPDATE)
01-NOV-1997 (PEL. 35, LAST ANNOTATION UPDATE)
NEUFSONAL PROTIO-ONZOGENE TYPOSINE-FROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDOBAAC9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE: PSO0107; PROTEIN_KINASE_ATP; 1.
PPOSITE; PSO0109; PROTEIN_KINASE_IYP; 1.
PROSITE: PSS0011; PROTEIN_KINASE_DOM: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN TYROSINE PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60487 MW;
                                                         FOR RPREPETENTOAFLE 517
                                                                                                 241 DEDERFTFEYIQSFLE 256
                                                                                                                                                                             STANDAFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A43610; A43610.
HSSP; P00524; 1PRL.
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MGD; MGI:98397; SPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             540 AA;
                                                                                                                                                                                                                                                                                           (P60-SRC) (C-SRC).
                                                                                                                                                            T 12
SPCN_MOUSE
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PHISPHORYLATION (AUTO-) (H) SIMILARITY).
(16ARES95 CRC32)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 TERCESTRIBLEGGGTFSEVENGTWEGTTRVAIKTLKPGTMSPEAFLQFPQVGGGLHHLR 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TV-LIMAVVSEEPTYIVTEYMSKOSILDFIKGEMGRYIRIPOIVOMAAGIASSMAVVEKMM 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (2) YTHRUTRAANILWITWIYYKIADFGLARLIEDNEYTARGGAKEPIKWTANGAALYGHETI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9. YVHROLRAANTLVGENLVCKVADFGLARLJEDNEYTARGGAKFPIKWTAPEAALYGRETT 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           440 KROVWSBRILLIELITKIRVPYPRAMVNREVLAGVERSYRMPOPPDOPESLHOLMEGONEK 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIMALIN SHALLOWALN STRASE, FHLSPHLHYLATION, MAIN SHALLOWALN, SHALLMIN SHALLOWALN, SHILLARITY, STRICKELTY, MYSTSTATE (BT SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ] IPPESIBLEVKIAGSSPROBVWASTRNOSTÄKVÄRKTEKPETHMYPBAFLUSAGIMKKTRUPK (C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NITEST ATTER BES. 13:1747-1741(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1793; DB 1; Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prof. M. C. Cerve: 20: Mismatches 11: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HNGER T.E. MARDIS M.J., FERO J.B.;
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ATP (BY SIMILARITY),
                                                                                                                                                                                                                                                                        531 AA.
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ATT THEFTERY LISTER 254
                                                                                                                                                                                                                                             SIANDARID
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Rost Loral Similarity 87,0%.
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88889 801524: 1086.
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                                                                                                                                                                                                                  SETA_XENLA
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260 IPRDSLRLELKLGOGGFGEVWMGTWNGTTRVAIRTEFFTTMSFFALGLEALVERKLPHEK - 15
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PHOSPH GYLATEON (AUTO-) TOY STRILABITY:
Absorbing operate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSFERASE; ATP-BINDING; TYROSINE-PROTEIN KINASE; PROCHERINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.1 KSDVWSFGILLTELVTKGRVPVPGMVNERVFELVER VERFORENTER 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA; METAZOA; CHORDATA; VERTERRATA; TETRANGUA: AMERIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        440 KSDVWSFGILLTELTTKGRVPYPGMVNREVLJAGVERGYKMPCPHJKTRESLHRGJKG 18 00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 LVOLYAVVSEEPIYIVTEYMSKGSIIDET FOIMGRYTRIJOLVURAALIAS DOGG.
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                                                                                                                                                                                                                                                                                                                                                    01-7410.
01-77410.
01-FEB-1994 (PEL 28. LAST SECUENCE UPDATE)
01-NOV-1995 (REL 32. LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE SRC-1 (FC 2.7.1.112) (FAULSPOTE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.3%; Score 1793; in 1) (40.01), fig. Conservative 20; Mismatches 11; Indexs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  380 YVHRDLRAANILVGENĻVÇKVADFGLAPLIEPHEYTAKGSARFFIRMIAFEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILAPITY.
MYRISTATE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE: 89278134.
SIEBLE R.E., UNGER T.F., MARDIS M.J., FFROM J.E.
J. BIOL. CHEN. 254:10649-10653(1989).
-!-CATALYTIC ACTULITY: ATP - A PROTEIN INFOSINE PROTEIN TYROSINE PROFESSION CONTRACTOR CONTRACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SH3.
SH2
SH2
PROTEIN KINASE,
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                               5 41 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP: PO0524: 1PRL.
PROSITE: PS00107: PROTEIN_KINASE_ATP: 1
PROSITE: PS00109: PROTEIN_KINASE_TYR: 1
PROSITE: PS50011: PROTEIN_KINASE_TYR: 1
                                                                                                                                                                                                                                                                                                                               PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XENOPUS LAEVIS (AFRICAN CLAWED FROG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYRISTYLATION; SH3 DOMAIN; TYROSINE-PR-
INII_MET 0 0 0 BY SH2 DOMAIN.
LIPID 1 1 BY SIMILA
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59725 MW,
                                                                                                  500 DPEERPIFEYLQAFLE 515
                                                                                                                                                  241 DPDERPTFEYIOSFLE 256
                                                                                                                                                                                                                                                                                                              STANDARD;
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PROSITE; PS50002; SH3; 1.
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                                                                         SRC_CHICK STANDARD: PRI: 532 AA
100522: 201245: C02013*
21-00-1986 (REL. 01, CREALED)
11-00-1986 (REL. 32, LASI SROTHNE UPDAID)
15-00-1998 (REL. 35, LASI ANNOTATION UPDAID)
PR.I.-UMCUCHNE INLOLNE FRITTIN KINASE SPT (EG 2.7 1.112) (P60-SPC).
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FENG S., CHEN C.E., T. H. SIMINIT A. SCHPEIPER S.L.

SCIENCE DECLINELINATION OF PECCHOSED IS UNKNOWN. IT IS EXPRESS

-1 - FUNCTION. THE EUGELISM OF PECCHOSED IS UNKNOWN. IT IS EXPRESS

-1 - FUNCTION. THE EUGELS, AND WITH A HIGH DEGREE OF KINASE ACTIVITY, IN CEMIALN FULLY DIFFERENTIATED CELLS SUCH AS NEURONS, PLATELETS
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SOULD Kill, MCCOGEII J.K., COMPER T A . ROSS J.E., SHALLOWAY D.,
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COOPER J.A., COUTE K.L., CARTWRIGHT C.A., HUNTER SCIENCE JA1:1411-1414 (1996).
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HEDITIE, AGATAMIE
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MEDLINE, 92092397.
SWARI U.E., GREARMAN B., TRENTILTERY A.P., PUPPERINGON N.L., BISHOP I M.,
PROC. NAIL, ACAL, SOI, GLA, TRECTITAL ACAL, SOI, GLA, TRECTITAL ACAL, SOI, GLA, TRECTITAL ACAL, SOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KAMPS M.P., TAYEUR S.S., SHITUN B.M., NATURE 310:589-592(1984).
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CELL. BICL. 11:4165-4176(1991).
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MEDLINE, 06151652.
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EURAALLIA, HEINTIA, TH
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ELL 32:881-890(1983).
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TYROSINE-PROTEIN KINASE; PPOTO-ONCUGENE; PHOSPHORILATION:
TRANSFERASE; AIP-BINDING; MYHISHILATION, SH3 LOMAIN, SH2
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PHOSPHOPYLATION (BY PKC).
ATP (BY SIMILARITY).
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C-SRC TYROSINE KINASE.
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Copyright (2) loan-joak University of Edinburgh, V.K.
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AFY TAL METAZUAL CHORDATAL VERTEHRATAL TETRAPODAL AVEST NEGUNATHAE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H4. KSEVNSBRILLIHLITKCRVPYPSMVNKEVLDOVERSYRMPOPPECPESLHCHMITHER HUB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHURTRETUGE S.A., MANN M., KIEMERGA R.;
                                                                                              -PERKINGS (IMEMBLEEL 02, CREATED)
-PERKINGS (IMEMBLEEL 02, LAST SECUENCE CHUAIE)
51-JUN-1998 (IMEMBLEEL 02, LAST SECUENCE CHUAIE)
3ENE C-SRC PRODUCING PROIEIN PP60-C-SRC
THIS, HAND IS HOMOLOGOUS IN THE ROUS SARCOMA VIRUS GENE V-SRC.
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543 AA: 60610 MW: 00446FP3 CRC32;
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                                            PPELLMINARY;
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TAKENA T. HANAPISA H., FELL (2198)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              382 YVHEDLRAANILVGENLVCKVADFGLARLIEDNEYTAEOGAKFITKWIAFEAALYTHETT 141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      442 KSDVWSFGILLTELTTKGRVPYPGMVNHEVLIHUVER-TYPRMPATH BYTESSIHFJRMVER (),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *** LVGLYAVVSEEPIYIVTEYMSKGSLLDFLKGEM3KY1RLPOLVDMAAU1AS3MAYVEEMN ++;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 98.7%, Score 17%4; DB 1%; Schuth 64%;
Matches 227; Conservative 18; Mismatches 11; Hedels 0,
                                                                                                                                            HANAFUSA H.;
SUBMITTED (JUL-1995) TO EMBL/GENRANK/DDBJ DA1A BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MFDLINE, 83155664.
TAKEPA T., HANAFUSA H.;
CELL 32.881.890(1983).
PMRL; J00844. G901820;
PROSITE; PS00107; PROTEIN_KINASE_AIP;
FROSITE; PS00109; PROTEIN_KINASE_AIP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 DPDERPIPEY!OSFLE 256
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VIRIDAE, SS-RNA ENVELOPED VIRUSES, POSITIVE-STRAND, REHOVOES SEQUENCE FROM N.A.
STRAIN-PR2257.16;
MEDLINE: 95016532.
YAISULA B.A. GERYK J., SVOBCDA J., KYNCTCH A.V., CALCHY
DEZELEE P.;
SAN, WIRECL 75:2777-2781(1994).
EMH: 121974; GA47052.PROSITE: PS00109: PROTEIN_KINASE_ATP; 1. 01-NOV-1996 (TREMBLREL, OL, CREATED) 01-NOV-1996 (TREMBLREL, OL, LAST SEGUENCE DELATE) 01-JUN-1998 (TREMBLREL, O6, LAST ANNOTATION DEDATE) PROTEIN-TYROSINE KINASE. 65778 MW: AU2F2A78 CPC12; PRT; PRELIMINARY; PFAM, PF00069; pkinase. TYROSINE-PROTEIN KINASE. SEQUENCE 587 AA; 6577 AVIAN SARCOMA VIRUS PEAM; PF00017; SH2; PFAM; PF00018; SH3; LT 4 Q64817 Q64817; Query Match

92.4%; Score 1746, 14.

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TRANSFERASE;
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DOMAIN
NF_BIND
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Q07461;
                                                                                                                          000 XXMCTAXIBELE----
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                                                                                                                                                                                                                                                                                                                                                                                                                   THEFIRM TREALLYGRETT 180
                                                                                                                                                                                                                                                                                            61 LVPLYAVVSEEPTYIVTEFYTA, SELLDFLKFFFTKLEGLVDMAAGTADGMATIFFMY 120
                                                                                                                                                                                                                                                                                                                                                         ... JAKTPIKNIAPEAALYGREII 441
                                                                                                                                                                                                                                  322 LVGCURAVYSEENLY (VT) - FRAFLIDELT " "CXXLRIPPLYDWAA07ASGMAYVERM" 381
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                                                                                                          262 IPRESIMITVRIAGAMESEVANGTUNGTOUALKTIMPOTAKSEAFLOFAOVURKIPHEM 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----CPPECPESTHDIMCOCWRK
                                                                                                                                                                       1 IPRESIRIEVKIGGGG GOOGLANDER CITTIFFER POINMIPEAPLUEADIMEKIPHOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CERTEBRATA LEIPAPODA: MAMMALIA.
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Matches 227: Conservative 19: , smalches 11; Indels
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EURABIOTAL METAGONA (1)
EUTHERTAL BLOSMITAL
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est Iodal Similarity
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IISSUE-MESENCHYMAL:
PODGE T POTROT F.
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KASHUBA V.I., KAVSAN V.M., RYNDICH A.V., LAZCHKEVICH Z.V., ZCHAK S.V.
POPOV S.V., DOSTALOVA V., HLCZANEK I.:
MOL. BIOL. 27:269-278(1993).
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SIRAIN-PR-PSV-C:
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VIRTURE: SS-FNA ENVELOPED VIRUSES, PUSITIVE-STERNO: NEIR VIRTURE.
ONCOVIRTURE.
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                                01-NOV-1996 (IREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL 01, LAST SECCIENCE UPDATE)
01-170N-1999 (TERMBLPEL 06, LAST ANNOTALLON UPPATE)
11-15.NET-PROTEIN KINASE TRANSFORMING PROTEIN SHOT (EC 2.7.11.112)
(P60-SEC).
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PFAM: PF00018; CNCOSENE.
FYRORINE-PROTEIN KINASE: IRANSFORMING FALIEIN CNCOSENE.
TYRORINE-PROTEIN KINASE: TRANSFORMING: WIFISITALION: TRANSFERASE: PROSPHORYLATION: ATP BINDING: WIFISITALION:
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Best Local Similarity 87.1%;
Matches 222; Conservative
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            PRELIMINARY:
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191 KSDVWSFGILLTELVIKGRVPYPGMVNREVLEQVERGYRMFCPQGCPESLHELMKLCWKK 240
                                                                                                                                            44.2 KSOWASFGILLIZITEGPUPTPOMWERP/LOOVENSYPHE/SPECEFELHALEGGGGGF 54.3
THEOLOGICAL AND STANDING SAFETY AND THE SAFETY WAS AND SAFETY AND SAFETY AND SAFETY OF THE SAFETY OF
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87.58: Pred No. 0 006-00;
vative 15: Mismatches 17: Indels 0: Gaps
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BERANCIA, HITAKOA, CHORCATA, VERTERRATA, TETRAPODA, MAMMALIA,
FTHERIA: RODENIIA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORALACET K . NEGOT F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | FEB. | FREIMINARY: FRT: 537 AA. | CZEATE: | CREATED: | CNIV. | CAUSTION (TREMELEE) | CLIAST SPOUENCE 'PDATE: | CAUSTION (TREMELEE) | CLIAST SPOUENCE 'PDATE: | CAUSTION (TREMELEE) | CAUSTION (TREME
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STRAIN-SHESP SIR-YES-PRONE SPUNIANEOUSLY HUDFRSENSIVE.
TISSTE-WHOLE HEALK.
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PROSITED PSCOOT PROTEIN_XINASE_ATP. 1
PROVIDED PSCOOT SHOT PSCOOT PSCO
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THEREZIAL VERTERATAL LETRAPODAL MANMALLA.

CLAZA FREDMINARY: PRT: 534 AA. CLEEMINERD: CL CREATE; SACRACE UPDATE; N. V. 1994 (TREWRIBED: CL CAST SECTION DEDATE)

N. V. 1994 (TREWRIBED: CL CAST SECTION DEDATE)

HTM SAFIENS (HTMAN) FTKARYTA: METANIA;

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443 KSDVWSFGILLTELVIKGRVPYPCMNNKHVLECVERGYRMFGFGATGSTHELMIHFTRK ? ...
                                                                                                                                                                                                                                                                                                                                                                                                                         263 VARPSECEEKKEGOGGFAEVWEGTWNGNTKVAIKTEKFGTMSFESFEEFASTRAKEREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 YIHRDLRAANILVGDNLVCRIADFGLARLIEDNEYTARGMAKFFIKWIAFFAANIXMET.
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                                                                                                                                                                                                                                                                                                                                    Match
221 Similatity 87.1%; Pred. No. 0.00c 002
7 223; Conservative 15; Mismatch...
88.7%; Score 1723; DH 14; Lemin F2
85.5%; Pred. No. 0.00e-00;
Vative 21; Mismatches 16; Indels
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01-NOV-1996 (TREMBLREL: 01, CREATED)
01-NOV-1996 (TREMBLREL: 01, LAST SEGUENCE CHEMATE)
01-JUN-1998 (TREMBLREL: 06, LAST ANW (A110) UPCATE)
                                                                                                                                                                          PEAM: PF00017: SH2
PFAM: PF00018: SH3.
PFAM: PF00069: PKinase.
SEOUENCE 534 AA: 60226 MW: D:941652 PF732:
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SEOUENCE 526 AA; 59148 MW; 0792DBCF CRC32;
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EMBL: S74774: G802051;
PROSITE: PS00107: PROTEIN_KINASE_AIP;
PROSITE: PS00109; PROTEIN_KINASE_IYE;
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REDRY S. MAZZU D., MAHAN D. SHALLSWATT

V.KELL 64:3545-3550(1990).

FRUSTIE, 220-271.

FRUSTIE, PSUGIU7: PROTEIN_KINASE_ATF;

PROSITE: PSUGIO9: PROTEIN_KINASE_ATF;

FRAN: PFOROIT: SH2.
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les 218; Conservative
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ROUS SARCOMA VIPUS
VIRIDAE: SS-RNA ENVELOPED VIRUSES: PUSITIVE-SIRAND; RETPOVIPIDAE:
VIRIDAE: SS-RNA ENVELOPED VIRUSES:
                                                                       382 YVHROLKAANILVGENLVCKVADFGLARLIDDNEVIARGGAKFPIKWIAPBAALYGRFTI 441
                                                                                                                                     442 MSTVMSFGILLTELTTKGFMPYPGMGNGEVLDRVERGYRMPGFPTG9ESLHDLMGGGWRR 501
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ANTINOPTERSOIL: ATHRRINIPORMES, CHISINODONIGIEEL: FUEITHITAE
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036352:
01-NOV-1990 (TREMBLEEL: 01, LASI SEQUENCE UPDATE)
01-UNV-1996 (TREMBLREEL: 06, LASI ANNIATION UPDATE)
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282 JPRESIRLEVKLGOGGFGEVMMGTWNGTTRVALKTLKPGTMSPEAFLOEAQVMKKLRHEK 342
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VIRIDAE: SS-RNA ENVELOPED VIRUSES: PUSILLVE-SLAAMI, RETROVIRLDAE:
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MELLHE: 96182936.
TATOSYAN A., YATSULA B., SHIUTMAN M., MOINGVA E., FAVERINA I.
TATOSYAN A., YATSULA B., MIZENINA G., ZUEVA E., CALOTHY G.,
MUSATKINA E., LESKOV K., MIZENINA G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.3%; Score 1710; LB 14, Length 546; Local Similarity 85.1%; Fred. No. 2 504-302; and as 217; Conservative 11; Mismatches 17; Indels C
SEQUENCE FROM N.A.
MEDLINE: 96182936.
TATOSYAN A., YAISULA B., SHTUTMAN M., MOINOVA E., KAVERINA I...
MUSATKINA E., LESKUV K., MIZENINA O., ZUEVA E., CALCTHY G...
DEZELEE P.:
                                                                                                                                                                                                                                                                                                                            Length 545:
                                                                                                                                                                                                                                                                                                                            Query Match 88.3%; Score 1715; UB 14: Length 5-Best Local Similarity 84.7%; Pred. No. 3.95e-302: Matches 216; Conservative 22; Mismatches 17: Indels
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01, LAST SEQUENCE UPDATED
06, LAST ANNOTATION TEPATED
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VIENLONY 216:347-356(1995).
VIENLONY 216:347-356(3086) - .
PROSITE: PSO0107; PROTEIN KINASE_AIP: 1.
PROSITE: PSO0109; PROTEIN_KINASE_IYR: 1.
PRAM; PRO0017; SH2.
PEAM; PRO0018: SH3.
PEAM; PRO0069; PKinase.
SEQUENCE 546 AA; 61105 MM: A80084E5 CRC32:
                                                                                                                                      DEALLER T. 6:347-356(1996).
VIEGLOGY 216:347-356(1996).
PROJETTE NOTOTO: PROTEIN KINASE_ATF: 1.
PROSITE: PSO0109: PROTEIN_KINASE_IYE: 1.
PRAM: PF000019: SH3.
FPAM: PF000018: SH3.
FPAM: PF000018: SH3.
FPAM: PF000069: PKinase.
SEQUENCE 545 AA: 61037 MW; D53537B6 CRC32:
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086363
086363,
086363,
01-W-V-1996 (TREMBLREL, 01
01-JUN-1998 (TREMBLREL, 06
pp62V.
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Thu Jan 14 13:43:25 1999

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US-08-955-841-4.rspt
                            THE TRANSPORT OF THE PROPERTY 
                                                                                                                                                                                                                                                                                                                                                                         452 YVHRDLRAANILVGENLECKVADFGLARLIEDNEYTARQGAKFPAKHTAPEAGLYGRFTI 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE RECOVERSE GLEEL SELVING REVERENCE OF THE THEORY STATES OF STREET HELD THE THE THE TAGENT THE THEORY STATES OF STREET WILLIAMEN THE THE THEORY STATES OF STREET WILLIAMEN THE THE THEORY STATES OF STREET WILLIAMEN THE THEORY STATES OF THE THEORY STATES OF THE THEORY STATES OF THE THEORY STATES OF THE THE THEORY STATES OF THE THE THEORY STATES OF THE THE THEORY STATES OF THE THEORY STATES OF THE THEORY STATES OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *22 :VOLYAVVSEEPTYIVIEYMSKGSLLNFLKGEMGKYLRLPQLVDMAAOIASSMAYVEKMN 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 JVPLYAAVVSEEPTYTVTEFMTKGSLLDFLKBGEGRFLKLPOLVDMAAQIADGMAYIERMN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *±2 YVHRDLRAANILVGENEVCKVADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTI 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | TPRESCRIEVRIGGGGFGFWMGTWNGTTRVAIRTERPGIMMPEAFLOEAGTKKFFFFFFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Crory Match
Host Local Similarity Rolls, Fred. No. 2.43e-301,
Matches 217; Conservative 22; Mismatches 16; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CREATED)
LAST SEGUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SZP AA: 58978 MW; BA716C43 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24: DPDERPTPRYIOSFL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           502 DPEERPTERALUADE 516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RUTS SARCOMA VIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM: PF00017; SHZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEDUENCE FROM N.A. KIRTRA V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM: PF00018; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IYROSINE KINASE.
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262 IPRESLRLEVKLGQGCFGEVMMGTWNGTTRVAIKTLKPGTMSPEAFLOFACVMKKLIHHEK (.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              379 YVHKOLRAANTLVGENLVCKVADFOLARI TITTITTARÇQAKEFTANTAFFAAATSTRFLL 4 OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 YIHRDERAANIEVGDNEVCKIADFGLAREIEDNEYTARGSAKEPIKWYAFFAALYDRUTT : ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       439 KSDVWSFGILLIELTIKGRMPYPGMGNGEVLDRVERGYRMPCPPB/TPFST HIGLMT27HFR 40H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match . 87.9%; Score 1708; DB 14; Lenath 524;
Best Local Similarity 86.3%; Pred No. 9.5le-301;
Matches 220; Conservative 20; Mismatches 12; Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Medical Maria Services and sections we seemed a service section of the section of
                                                                                                NISHIZAWA M., MAYER B.J., TAKEYA T., YAMAMOTO T., TOYOSHIMA F.,
                                                                                                                                                                                                                                                                                                                                                                                              FFAM; PE00059; PKinase.
SEQUENCE 523 AA; 58742 MW; 2C76C501 CRC32;
                                                                                                                                                                 PROBLEM CONTROL SECTION CONTROL SECTION CONTROL MILES CAROLAGE CONTROL MILES PSOULOT: PROPERLY FINASE_ATP: 1. PROSITE: PSOULOG: PROTEIN_KINASE_ATP: 1.
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                                                                                                                                                                                                                                                                                                                                  PFAM: PF00017; SH2.
PFAM: PF00018; SH3.
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FELINE SARCOMA VIRUS (GAPDNER-ARNSTEIN FELINE (FEREMIA (NO VICE)) VIRIDAE: SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND: RETROCCES, AND AND STRANDE RETROCCES.

Match Local Similarity 79.3%; Pred. No. 4.55-278; es 203; Conservative 25; Mismand 1.55.

Query Match Matches

-W-V-1996 (THEMRIREL. 01, CREATED)
-W-V-1996 (THEMRIREL. 01, IAST SECUENCE UPDATE)
SET ANNOTATION UPDATE)

ROTS SARCOMA VIRUS.

PPAM: PF00069; pkinase.
POLYPROTEIN, STRUCTURAL PROTEIN.
SEQUENCE 663 AA: 74916 MW: F6B1A6410 CHC32;

PFAM; PF00017; SH2. PFAM; PF00022; Jetin.

MEDLINE; 84097512.

NAHARPO G. ROBRING K.C., REDDY P.E., SCIENCE 223.63-06/1984).

EMBL; KO1487; G323895,

PROSITE; PSO0107; PROTEIN KINASE_ATP; 1.

PROSITE; PSO0109; PROTEIN_KINASE_ATP; 1.

PROSITE; PSO0132; ACTINS_ACT_LIKE; 1.

SEQUENCE FROM N.A.

399 ISRSSITLORRLGTGCFGDVWLGMWNGSJKVAVKTJKFFTJMSPKASTTV

inders

Mismatches 27;

01-JAN-1998 (TREMBLEE, 05, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLEE, 06, LAST SEQUENCE UPDATE)
03-ROHER-RASHEED FELINE SARCOMA VIRUS
(GR-FESV) V-FGR ONCOGENE CODING FOR P70-GAN-FGR TRANSPY-PMING FOR

553 AA.

PRT;

01-JAN-1998 (TREMBLREL, 05, CREATED)

PRELIMINARY;

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HISENGENIST 1.0 [Notice of by Wisconskill of the margh, then obeauges these 1969 from 1 to: 1769

Satabase Release Information: GenBank, Release 109.0, Released on 15oct1998, Formatted on 17oct1998 EXML, Release 56.0, Released on 16Sep1998, Formatted on 18oct1998

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GB_PR2:HSU40282	+	О			U40282 Homo sapiens integrin-linked
MC9447	•	-43	604	ىد.	9 Mus musculus integrin
8:319940	1	0 ·	150	CI	human STS A002C40, sed
GB_PR2:HSU25916	٠	0000	93		Human TATA binding protein a
38_PR2:HSU25816	1	2385	63	C1	Human TATA-binding
G8_818.G1994.9		0	~	e 1	COOM SIS WEMEN
33_PR2:AF013988	+	-354	31		3 Homo sapiens seri
	•	. I	ci i	r + .	4. sapiens mRNA for peroxisc
GB_PK1:HSU13991	I	707	29	۲.	2
	•	1	യ		ALC09010 Flasmodium falciparum DNA *
38_F1:A8010073	•	37257	رم 80	0	AB010073 Arabidopsis thaliana genomi
GB_PR2:AF033242	•	CI CI	ထ		AF033343 Macaca mulatta peroxisome p
GB_PR2:AF033342	+	(C)	C1 80		AF033342 Macaca mulatta peroxisome p
CB_FR2:AF033103	•	67.	64 89		AF033103 Macaca mulatta peroxisome
GB_HTG:AC005170	+	35287	28	σ	AC005170 *** SEQUENCING IN PROGRESS
CB_IN:DOSTATOUT	,	100	(·)		Y13098 D. discoideum mRNA for stat pr
C0ECT22:32:35T080	•	1437	57	3	513973 Dictyostelium discoideum Dp87
3B38_350660000	•	-1004	[·		AF668225 Orbithodoros moubata ferrit
3B_0V:0LJ000938	•	392	27		AJ000938 Oryzias latipes, Pax6 gene.
OBLIN: PYYELS	1	1704	27	-1	X55197 F.yoelii YEL6 gene for ATPase
GE_FR2.ACCCCCT	•	34333	r> CI		AC002351 Homo sapiens 12924 PAC RPCI1
GB_HTG:AC005505	,	98887	27	Н	AC005505 *** SEQUENCING IN PROGRESS
GB_HTG:AC005489	•	12072	27	S	AC005489 *** SEQUENCING IN PROGRESS
GB_PAI:122011	٠	-1717	C1	64	122011 Sequence 97 from patent US 55
GB_P12:AB016889	1	54055	7.7	13	AB016889 Arabidopsis thaliana genomi
GB_IN:DDIDP87	4	.865	36	11	D13973 Dictyostelium discoideum Dp87
GB_IN:D82024	1	832	e G	17	D82024 Dictyostelium discoideum DNA
GB_IN:AF052833	٠	19397	90	97	AF052833 Trypanosoma cruzi CL Brenei
GB_OV:XEHAND	+	-508	52	C1	295080 X.laevis mRNA for eHAND prote
GB_CV:OTISLIMRA	+	-188	36	ω	X64882 O.tschawytscha isl·1 mRNÅ. 7,
GB_:V:AF014366	•	945	56	9	AF014366 Danio rerio transcription
CB_IN:PESCO4086	•	2138	9	11	AL010273 Flasmodium falciparum DNA
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ションフター・・・	•)	1171	2 K	٠, ۲	ALUUSJOS Flasmodium Ialciparum DNA **
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GB IN: PEMALSP?	•	40.00	100	, c:	798547 Plasmodium falcinarum MAL3D3
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GB_8T8:333984	•	C)	93	10	G37984 c3m58 Plasmodium falciparum ha
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(Nucleotide) WPPDSEAPTH of Ahrme/maryh/chen.gog chook: 2569 from: 1 to: 1789 TO: GenEMBL: * Sequences: 567,306 Total-length: 1,118,886,981 January 13,

 701 TGAACAAACAGICIGGCATIGACIICAAACAGGIIAAGIIGGIGAGGAAG 750

601 CGAGAGGGGGAGAGAAGATGGGGCCAGAALCTCAACCGTATICCAIACAA 650

Database Release Information: GenBank, Folgase 102.0, Released on 150ct1998, Formatted on 170ct1998

Then.gdg to 1789 there 272 from 1 to 1789 there 272 from 1 to 1789 there 272 from 1 to 1784 Home Sapiens integrin-likes Kinsse (11K) mHIA, complete days 50 qaps: 0 Quality: 17874 Ratio. 9.991 Score. 1788 Width, 9 Limits. 7/10 EMBL, Pelease 56 0, Peleased on 16Sep1998. Pormatted on 18Oct1398 2,000,000,000 AvMatih 3.84 AvMisMatch: 18.00 SapWeight, 50 LengthWeight: 3 351 IGGGGAIGACACCCCCCTGCATCIGGCAGACAATCATGGACACACGTGATA 400 51 CAGCCCGAGICCCGAGGATAAAGCITGSGGITCATCCICCTICCCIGGAI 100 GIGGIIGAGAIGIIGAICAIGCGGGGGGGGCACGGAICAAIGAACCG 350 301 GIGGIIGAGATGIIGALCAIGGGGGGGGAAGGAICAALGIAALGAACCG 350 551 AIGGAGAGAIGCCIGIGGACAAAGCCAAGGCACCCIGAGAGAGCIIC eUU 601 CGAGAGGGGGGAGAGAAGAIGGGGGGAGAATCICAAACGGIAIICCAIACAA 650 1 GAAIICAICIGIGGACTGCTACCACGGGAGITGCCCGGGAGAAGGATGCTG 50 1 GANTICALCIGICGACIGCIACCACGGGAGITCCCCGGGAGAAGGAICCIG 50 101 CANTOCACASTCOTCAGGOTTCCCCAATCCAGGGGACTCGGGGGCCCGGGAC 201 OSITOSCORGOSCIGOACAGAGAGAGAGAGACGIGAAGIASSSSSACC 451 CACGGGAATGTGCCCCCTGCACTATGCCTGTTTTGGGGGCCAAGA1CAAGT GGCAGAGGACTGGIGGCAAATGGGGCCCTIGICAGCAICIGIAACAAGT 551 AIGGAGASAFST FSTSSAVAAASCAASSCOOLISASASASLICIC 151 GCIGCIAIGGACGACATITICACICAGIGCGGGAGGGGAAGGCAGICGC 251 ATCAIGGCIICTCCCCCTTGCACTGGGGCCTGCCGAGAGGGGCCTGTGCC Match display thresholds for the alignment(s): - IDENTITY chen.gc3 GE_FF2·HSU40282

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                                                                                                                                                                                                                                                  412 TGAAGGTGGTGAAGGTTGGAGACTGGAGTACAAGGAAGAGCAGGAGGTTC 861
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1576 GAGG 1573

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GB_PLI:AB010073 check: 4255 from: 37257 to, 80076
AB010073 Arabidopsis thaliana genomic DNA, chromosome 5, Fl ciones MFN.: eventse
Gaps: 0 Quality: 314 Ratio: 7.659 Score. 28 Width. 10 Limits. 7.11
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GB_PRSAR033343 cancer: 9613 from: 12 to: 1769
AF033343 Macara milatha peroxisome proliferator activated receptor crimes 1.1: (19
Gaps: 0 Ouality: 286 Ratio: 6.651 Score: 28 Width W. Limits 7.4:
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ASB C Gualliy INK Faith Act Soit 28 Wilth C 1801 C.
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IB_IN:POTEPR9 check: 1426 from: 1 to: 4468
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Sags: 0 goality: 246 Patis: 9 222 Secte: 27 Width: 0 (1917)
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OP_PRINTPARCAM check: 2569 from: 1 to: 1769

Caps: 1 condition FPA Tricks from: 1 to: 1767

Caps: 1 condition 276 Parion 5.727 Score: 29 Width: 21 Limits: 1762
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HyppyApr
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chack: 7000 from 1
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                                     Check: 2569 from: 1
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A0000938 Oryzias latipus: Park grow 7598
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BHIG ACOC489 Check: 14644 from: 1212 to: 101844

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GR_HTG.AG05505 check: 4490 from: 98887 to: 160964
AG05505 *** SEIGENATING IN PROGRES *** Plasmodion in interval to the content of Gaps. 0 Quality: 276 Fatto Pile Serie 27 William in interval.
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cH_ASAPO14466 check 2483 from 445 to 274
Asaps: 0 chall ty: 404 Ratio: 7.600 Score: 26 Width: 9 Limits: 47-10
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chen.gcg check: 2569 from: 1 to: 1789 /Ferense: RefeEAN1 check: 4716 from: 1171 to: 468 from: 1770 from: 468 from: 1171 from: 468 from: 1771 fr
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GALINE PPAPESAMUI belock: 524 from: 140 to: 186
M28195 Plasmodium falciparam (1804-02 FCR3) fiberinfected orythrocytes situate and
Gaps: 0 quality: 260 Ratio: 19:000 Score. 26 Width. 12 minits. 77 [1
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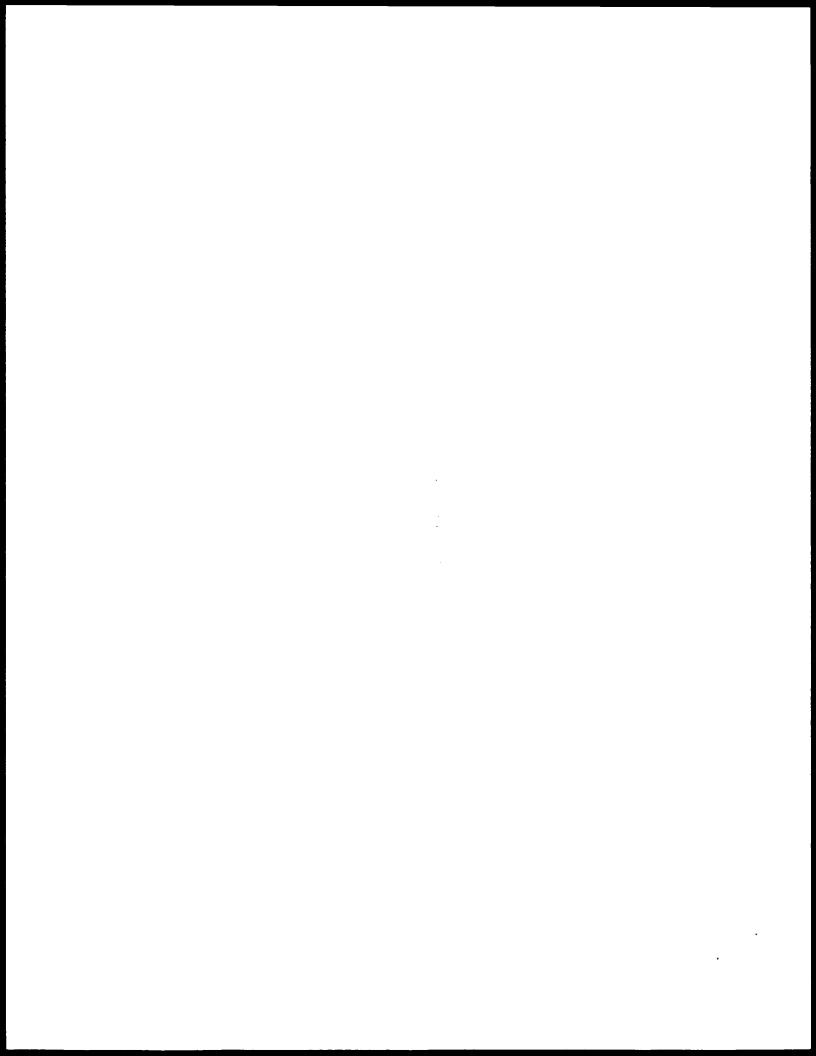
P_IN:PESCO3017 check: 74.7 from: 2027 **: 27.07

10.08969 Plasmodium falcipartm DNA *** SEQUENTING IN FFFFFESS *** [10.0807] 1 to 55.5 ft with the relations of the check of t
hon grq check: 2564 from: 1 to: 1744 /westso
BE_IN:PFSC03017 check: 7417 from: 27152 to: 27207
ALG08969 Flasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from confid
Caps C Quality 278 Fati: 9 0f8 propor 26 Wilth G [1975 c] to
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BR_INEMOSDUC check: 9893 from: 1474 to: 7252

INTROBUSDUC check: 9893 from: 1593 b.melanogaster (505) 303etis, submit 6 perteciped according ages: 6 gralling: 286 Fatic: 7.778 Secret: 26 Width: 6 timile: 7.778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298547 Flasmodium fulcipatum MALNES, complete acquara 1977 saps: 0 grality, 264 Batto, 9,429 Secre. 26 Wilth, 12 Chille, 77 Chil
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GB_NSPEPOLD check, 4720 from: 1920 + 0.0 827
XECAS F.I.Siparum.poldolta gene for DNA polymeran dillu.572
Gaps: 0 Quality: 256 Ratio: 10.000 score: 26 Width, 9 Mailts.72
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N.EMALFADAE check: 4845 from: 1870 to: 4668
N.EMALFADAE check: 4845 from: 1870 to: 4668
N.14932 D.melten-gaster eRAN for taplata-daptic base.co. q. 1577
S. D. Quallity 272 Frait, 1971 searce, 20 William 18 (1871)
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chen.gcd check: 2559 from: 1 to: 1789 /Reverse check: 3521 from: 52 to: 307 check: 3521 from: 52 to: 307 check: 3521 from: 52 check: 367 check: 3521 from: 52 check: 367 check: 367 check: 360 check: 360 check: 360 check: 360 check: 4/-11
Check. 2569 from: 1 to: 1789
3H_FLIAFPOTOTS Check: 255 from: 2569 to: 4367
AF\077793 Zea mays retinoblastoma-related protein 1 (RRM) mRNA, complete cds. 9/
GPP*** AP\077793 Zea mays retinoblastoma-related protein 1 (RRM) mRNA, complete cds. 9/
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38_PR2:HSU97680 check: 6241 from: 1 to: 1462
097680 Homo sapieus cycliu Al mRNA, partial eds. 6/97
3aps: 1 20318ty: 200 Patin: 7 179 Seare: 26 Width: 8 Limits: +/-9
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AC005170 *** SEQUENCING IN PROGRESS *
122011 Sequence 97 Ltom patent US 552
A7000938 Organs latipes, Pax6 gene.
X55197 P.ycolli YEL6 gene for ATPRSC
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AF068225 Ornithodoros moubata ferriti
AC007351 Henro sapiens 1242 FAC FPCII
AC005505 *** SEQUENCING IN PROGRESS *
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JOSTSTOTOCOAACAISSSASSASSASOCOGOCOTOTOCACAALAAAGT 1759 	Tattatgaanaaaaaaaaaaaaaaa 1789 	check, 2569 from R2 (* 1759 / Reverse check: 7000 from: 1 to: 222 (* 1764), sequence tagged site 7/96 (* 1835 Robity: 1835 Ratio: 8 ML2 Spore: 150 Width: 2 limite: 7/100	ODITGAROCORODOCTOTTGOSGACASIGEROSGACORRA 1644 	obacocca jostrossatastaccatcaciosacsossacaccacca 1895 	GAGGOGIGOTIOGGGGGGGGGATTCCCCGAACALGICCCGAACAC 1545 	TOTOGRAPHICAGGGAAGGACTTOCAGTOCHAGTTGTOCHGCATCTTCTC 1495 HILLIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHITHIHI TCIGGAGTTCAGGGAAGGACCTTCCAGTCCTACHGICCGGCALCHAGCAT	ACCATAGG 1486 ACCATAGG 222	check: 2569 from: 39 to: 1789 check: 1077 from: 1 to: 1750 # Mus muscilus integris: biology protocn kindsompsKA compacts income of parties of the protocn from the second from	OSCAAGAGGGC.GGGCTCAGAGCTIGICACTIGCCACA GGIGIOLOC 1720 	CAACAIGSSAAGGSAICASCCCCGCCIGICACAAIAAAGIIIAIIAIGAAA 1770 	AAAAAAAAAAAAAA 1789 	check: 2569 from: 1 to: 1769 /Recerse check: 4430 from 1885 to: 2605 check: 4430 from 1885 to: 2605 check: 4430 from 2885 to: 2605 check: 430 (1AF) 130 (1AF) cene, comparability: 1019 Satio: 7:511 Secre. 38 Willing 1 infine: 7:7	TITITICATAATAAATITAITGIGAAAAGGGGGGGGGGTCCCTCCCATG 1724 	TEGGGGGGGGAGATGGGGAGGGGAAGTGTGAGGGGGGGGG	OGGAÇASTGASTATGSONGAAGOGĞATGSACONO 1637 	093407 (K)
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1773 ITTITICATAATAAACTITATIGIGAGAGGGGGGGGGGGCGCCCCCCAIG 1724

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chen grg check: 2569 from: 1 to: 1704 /9000180
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ABG10072 Arabidopsis thaliama genomic DNA, chromosome [, F] check the free check gaps: 0 Quality: 314 Ratio: 7.659 Secre: 28 Width: 1 Limite: 7/ L
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AF033342 Macaca mulatta peroxisome proliferator activated receptor sampa [54 (H) 65ps: 0 Quality: 284 Ratio: 6.651 Score. 28 Wilth: [16:11.07.07]
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Statistics: Neur 33,246, Variance 136,336, scale 0,243

a-geneseg32 1:part1 D.part2 3.part2 4.part4 5:part5 6.part6 7.part3 8:part1 10.part9 10.part10 11.part11 10.part12 13.part13 14:part14 15:part2 26.part2 17:part3 26.part2 24:part24 26:part26 21:part21 20.part22 23:part23 25:part29

Minimum Match 0% Listing first 45 summaries

Post-processing:

Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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activating activity for use as cancer blorapy.

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                                                        N-terminal truncated cytoplsmic tyrosine kinase. cytoplasmic, tyrosine kinase, blood, cell differentiation; soreening, anticancer agent, SH3, sic homology domain.
                                                                                                                                                                81.155
/note- "SH2 domain"
192.438
/note- "tyrosine kinase domain"
                                                                                                                      Location/Qualifiers 7..70
                                                                                                                                              /note= "SH3 domain"
           R71132 standard, Protein, 466 AA.
R71132;
                                                                                                                                                                                                                                                         25-AVG-1994; J01411.
25-AVG-1993; JP-21403.
29-MAR-1994; JP-058553.
(ASAH ) ASAHI KASEI KOGYO KK.
                                          27-0CT-1995 (first entry)
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WP1; 95-106842/14.
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Query Maton 61.1%; Socre 1159; DF 12: Length 466; Best Local Similarity 58.3%; Fred. No. 5.04e-104; Matches 147; Conservative 31; Mismatohus 12; Indels 2: Jug

190 nlqhltlgaqigegefgavlqgeylqqkrarknikodkodrayafldetarmikmqherler 🕜

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Prosine kinase showing 48 homology with csk. It appears to play
a requidecty role in the growth and differentiation
medakarovers and perhaps neural tissues. Recombinat MMV1 as P.

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21-AFF-1945, US-225545,
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te= "SH2 domain"
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25-AUG-1993; JP-210403,
29-MAR-1994; JP-058553,
(ASAH ) ASAHI KASEI KOGYO KK,
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ULT 4 R71131 standard; Protein; 246 AA. R71131;

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Fred. Ho. 7.026-102,
43. Mismatches 50, Indels 2, Caps
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11.FEB-1752 (Lirst Folly)
AFRECH Folused Seno. A transcript.
A.c. Sch. Foluses: Therapy: timour, abl protoconcogene.
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12-MAR-1984: USL4II.
25-MUG-1983: UP-210403.
24-MAR-1944: UP-058553.
(ASAR-) ASARI MASEI MOGNO MM.
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Wossisins-A.
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                                                                                                                                                                                                                                                                                                                                                                                                        119 NNFVHRDIAARNVIVSEDNVAKVSDFSLTV--EASS-JORTG-KLRVKWTAPEALREKKF (7)
kinase encoding family of genes. And is expressed as two transcripts By analogy with c-abl, the alternative 5 and sequences have been designated A and B (014937) and it is assumed that they are joined to the ang second exon the among second exon Sequence is represented as found in the specification.
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                                                                                                                                  Match
Local Similarity 47.7%; Pred. No. 6.82e-77;
es 123; Conservative 61; Mismatches 56; Indels 8: Gaps
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Disclosure, Fage 28-29; 40pp; English.

Disclosure, Rage 28-29; 40pp; English.

Disclosure, Rage 28-29; 40pp; English.

Disclosure, Rage 28-29; 40pp; English.

Rinase was compared with the sequences of 3 members of a newly-identified non-receptor tyrosine kinase family. ATK / M945%; ITK (19945%) and TEC (19945%), and with novel human cytoplasmic tyrosine kinase BMX (see also 8945%). Close human cytoplasmic
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Drosophila Src28C tyrosine kinase.
Cytchlasmin tyrnsine kinase; BMX: haematopoietic cell:
Cytchlasmin tyrnsine kinase; BMX: haematopoietic cell:
Cytchlasmin tyrnsine kinase; BMX: haematopoietic cell:
Src28C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Autophosphorylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label = Tyrosine-Kinase_domain
187..209
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07-0CT-1994; VS-320432
(UVHE.) UNIV HELSINKI LICENSING LID OY.
Alitalo K;
WPI; 96-209856/21.
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Key
Location/Qualifiers
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Alabel SH3_domain
/label SH3_domain
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| Tabel = SH2_domain
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P94538 standard, Protein; 441 AA.
R94538;
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                                                                                                      62 UNVIVERKOULTIVTETMAKGSLVDYLRSRGRSVLGG-DCLLKFSLDVGBAMEYLEGNNF 120
                                                                                                                                       249 Shrdiaarnelygsenyykvadfglaryylddusteesankffikksfftvilytilssk 558
                                                                                                                                                                          12: VHROLAARNVLVSEGAVAKVSGEGIR---EASSTODIG-KLÞVKWIAPEALHEKKESIK 176
                                                                                                                                                                                                             sow sdywayavimmoittogkmyyayikatejykiyyryryiiekpkscakejydymklowshg 418
                  4 FLKIIOTIGKGEFGEVMI,SDYRGN-KVAVKCEKNDATAQA-FLAEASVMTQLRHSNLVQL 61
                                                                                                                                                                                                                                                 SOVWSPQILAEITSFGRVF1PKIPLKDVVPRVEKGYKMDAPDGGPPAVYEVMKNOWHLD 236
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The human dark encoding this protein is closely related to but is still for the curvating this protein is closely related to but kinger encoding family of genes, Ara is expressed as two transmine by analogy with clab, the alternative for stransmission as two transcripts desumated A without and H and it is assumed that they are joined even.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60) Mismatches 69; Indels 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel buman gene related to the consoder of designated "Abeliann Ketated Gene", ara, useful for tumbur diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 830; DB 3; Length 1182;
Pred No 1.426-70,
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Arg. Hagmosis: therapy: tumour: abl prote uncognne
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815155
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                                                                                                                                                                                                                                                                                                                                                                                                                         12-PEB-1992 (first entry)
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Pst Local Similarity 46.3%;
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Cytoplasmic tyrosine kinase: BMX: Haematrycoleti. 1011;
Til glowth, ceil proliferation: tumour; diagnosis: Therupy: KIK.
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Stimulate haematopoletic cell growth.

Cytoplasmic tyrosine kinase BTX (R9434) is scientively expressed at certain stages of B-cell devolpment. The sequences of HK kinase family. ITX (R84535) and TEC (R94536), and of the Drosophila Src28C tyrosine kinase (R94538), whre compared with that of novel cytoplasmic tyrosine kinase (R94538), where compared with the com
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Local Similarity 44.5%; Pred. No. 7.30e-70;
es 114; Conservative 56; Mismatchion 77
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09-0CT-1995; F10555.
07-0CT-1994; US-320432.
(UYHE-) UNIV HELSINKI LICENSING LTD UY.
Alitalo K;
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= SH3_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= SH2_domain
R94534 standard; Protein: 659 AA.
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W06708 standard; Protein; 659 AA.
                                                                                      10-JUL-1996 (first entry)
BIK tyrosine kinase.
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Sequence 659 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96-209856/21.
                                           R94534;
10-JUL-1996
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                                           ACCCCCS SPEED BRANCH SEED STATES OF SECOND S
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W06708; 04-FEB-1997 (first entry)

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Mouse haddalugedelicischertroted tyrosine Kraso.

Royner-Tyrosine Traine Kraso.

Royner-Tyrosine Traine Traine.

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R94535 The Control of                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signature (Section Constitution)
                                                                                                                                                                                                                                                                                                                                                                      27-AUG-1996.

4-DEC-1992: 985988.

21-CAN-1993: US-985998.

21-CAN-1993: US-505449.

21-CED-1995: US-901615.

(REG) UNIV CALIFORNIA.

(REG) UNIV CALIFORNIA.

WPI: 96-401601/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LIGVIVEERGOLYIVTEYMAKGSLVPYLFSFERSVLGGEGLLYFSLLVDLAMEYLEGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ។។ សែលក្រុមិទូសកម្មាយ ភេឌឆាមកព្រះមាន១០៩៩០១ក៏ដូច្នេះសំសុខសុខការក្រុមិទីព្រះខ្ពស់ខ្ពស់ខេត្តិទី២៥៩៩ខ្ពស់ស្ពស្តីខាន
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              479 In alasmonygengvikwsdfgmtrfvlädggresstgrkflavkststerfsfatterf
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TEC tyrosine kinase.
Cytoplasmic tyrosine kinase: BMX: haematopoketic cell:
cytoplasmic tyrosine kinase: Lambur, duagnosis, therapy: IEC.
                                                                                                                                                                                                                                                     Will delights the state of the second                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 41.9%, Score 796; DB 17; Length 62'; Local Similarity 44.4%; Pred. No. 4.05e-67; es 114; Conservative 61, Mismatches 72, Indels 10:
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/note= "the N-terminal region contains the
pleotstrin hemology region consisting
a 7-strand antiparallel beta-sheet"
184..236
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/label=_Tyrosine-kinase_domain
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18-ARR-1996.

03-007-1995. F10555.

03-007-1994. US-32042.

(UYHE-) UNIV HELSINKI LICENSING LID OY.
18-AEE-1996.
69-607-1995.
69-607-1394. US-326432.
(UVHE-) UNIV HELSINKI LICENSING LTD OX.
Alitalo K:
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246.344
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24-APP-[446] ***6708.
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Simulate haemacopoietic cell growth.

Claim 1: Page 19-21: 40pp: English.

Novel Cytoplasmic tyroshe kinase HMX (R9454) is rapuble of stimulating growth and/or proliferation of brownings is cells.

Simulating growth and/or proliferation of brownings is cells.

Fig. 18: EC (see R94538) at 18 useful as a modern for a cells.

Growth and differentiation and for various types of turning formation, and in the diagnosis and treatment it is series.
                                                                                                                                          4 ELKLLOTIĞKGEFĞDVMLGDYRĞN-KVAVKCIKNDATADA FILAFASVMIŞIFHLIN.
                                                                                                                416 eitlikelgsgafgavglgkwkggydvavkmikedsmswdc11goagramkiscjs
                                                                                                                                                                                                                                                                                         594 dywafgilmweyfsigkgpydlydnsqymlkysgaln lyrphlasaf tyginnysos.
                                                                                                                                                                        476 yavoskeyp-iyiyteyisngollnylrshqkg-lepsq)lomoydvoonmatt.
                                                                                                                                                                                                                                                                                                         122 HECLAARNILVSEDNVAKVSDFGLTKFASSTQ--DT-G-KLIPVKWTAFFARRES
                                                                          Length 675;
                                                               Score 770: DB 15; Lenath 475;
Pred. No. 1.77e-64;
58: Mismatches 81: Inde(s
                                                                                                                                                                                         (T90617), and used in the treatment and dramesis of real cakemia and thrombocytopenia.
                                                                                                                                                                                                                                534 hrdiaarnolvdrdlovkvsdfgmtryvlddgyvssvarktprevsaperii
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Cytoplasmic tyrosine kinase BMX and related DMA - usering ex-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= N-terminal_region
/note= "the N-terminal region contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pleckstrin homology region consisting of a 7-strand antiparallel hetassigner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytopiasmic tyrosine kinase, BMX: haematopoietie eet cell growth, cell proliferation; tymour; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label- Autophosphorylation_site
/note- "corresponds to the Tyr4!e
autophosphorylation site of c-Ster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Tyrosine-kinase_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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/label= SH2_domuin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= SH3_domain
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R94533;
                                                                                                                                                                                                                                                                                                                                               654 ekrptfggllssieplrekd 673
                                                                                                                                                                                                                                                                                                                                                                            238 AMRPSFLOLREQLEHIKTHE 257
                                                         Match 40.6%;
Local Similarity 43.5%;
Res 113: Conservative
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09-OCT-1995; FI0555.
07-OCT-1994; US-3204
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                                                                                                                                                                                                                             476 jgroskojp-ij/ujerisngellngilxshgkg.lupsqllemcydrocgmafleshqfi 533
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                                                                                                                                                                                                                                                                                                                                                                                                                                        179 DVWSFGILLWEITSFGRVPTFRIFIKDVVPFVFRJTRMFAPDGGPPAVYEVMENGWHLDA 237
                                                                                                                                                                     4 ELECTOTIVE SECOND STREET FOR STANDARDA ALAEASVALILEESKLVQL 61
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                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fused polypeptide - has amino acid sequence of bota-galactusidase with a LCF york linjurated to the N Ferring via DNA haring multi-cloning site
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The sequence consists of the Noterninal amino acids of the beta-alacted sequence consists of the Noternina amino acids of the beta-alacted sequenced by Ecoli transformed with the let grow vector (see 013983). It is useful transformed with a recombinant vector (see 013983). It is useful transformed with a recombinant policy in mannersactive with recombine by grow-derived polypeption in I calls. The actibody may recombine by grow-derived polypeption in I calls. The actibody may sequence 417 AA.
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(Refergelantys12sts Nothemical)-(1s* game prod ) fusion profess.
                                                         atch 40.6%, start 770, DB 17, Length 675, 03 (Sfmilarity 42.5%) Prof 9- 1.70-64, Length 675, 113: Conservative 50, Mismatches 31, Indels 8;
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Prod Wo. 4.66c/63;
60; Mismatches 76; Indels
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Zhoto "beta-galantosidase fragment"
resulting from deregulated tyrusine phosphorylation
Sequence (675 AA)
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ĝi standard: Protein: 417 AA.
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Best Local Similarity 43.5%:
Matches III, Consernative
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28-DEC-1989, 338268.
28-DEC-1989, UP-338208.
(TOWT), TOWINAMA SODA MY
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N-PSDB: Q14231.
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                                                           Cuery Match
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Cloning of a Complementary DNA for a protein-tyrosine kinase
that specifically phosphorylates a negative requiatory site
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This protein lacks the N-myristylation and autophosphorylation sites present in src and its close relations.
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Plages, S., Adam, D., Class, K.: Faremoli, J.: Holem, J.:E.
Penhallow, R.C.
Proc. Natl. Acad. Sci. U.S.A. (1994) 912297-2864
Ctk: a protein tyrosine kinase related to CSK that defines a
enzyme family.
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#journal Neuron (1991) 6:691-704

#ittle An extended family of protein tyrosine kinase ne across-references Milb:9122256
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##residues 1-450 ##label NAD1
##cross-references EMBL:X58631; NID:q57507; F1L:u57508
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Righns, S., Adam, D.: Glass, K.: Fargholl, J.: Bolon, J.B.;
Ponhallow, R.C.
Proc. Nati. Acad. Soi. J.S.A. (1444, 91:2547-2401
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Chow, L.M.L., Jarvis, C.D., Hu, O.: Nyo, S.H.; Onyols, F.T., Veillette, A.; Matis, L.A.
Proc. Natl. Acad. Sci. U.S.A. (1994) 914075 4079
Ntk: A Csk-related protein-tyrosine kinase expressed in Feat.
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Two distinct protein isoforms are encoded by mrk, a
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Higashitsuji, H.; Nishiyama, H.; Tukeneka,
H.; Fujita, J.
Oncogene (1995) 10:945-952
Presence of alternative 5' univalsized error
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J. Nourosoi, Res. (1994) R8:705-715
Identification and Oberatferiration of Batk, a predominantly brain-specific non-recoptor protein tyrnsine kinase related
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#authors Movicar D.W.: Lal. B.K.: Lloyd, A.: Kawamura, M.: Chen, Y.O.: Zhang, X.: Staples, J.E.: Ortaido, J.R.: Cighos, J.C.: Apornal chocogene (1994) 9.1037-2044 #... Molecular Cloning of 18K, a carboxyl-terminal atc kinase #title (csk) related gene, expressed in lenkorytes.
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##residues 1-465 ##label RES
##cross-references GB:S71669; NID.9559593; PID:9559594
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53; Mismatches 53;
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Best Local Similarity 55.7%:
Matches 143; Conservative
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The selection of the seguine structure, and typosine kinase activity of the same property and typosine kinase activity of the same property of
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108; Pred. No. 4.866-193;
170 51; Mismatches 47; Indels 4; daps
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15-Nov-1984 #sequencc_revision 30-Sep-1989 #text_change
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##FORSSTOTOFORONS GRILLB9944 NO0455449 | PID:9459580
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Valoins 14:1 Comsonality
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kinase homology: SH2 homology: SH3 homology
ATP, autophosphorylation; phosphoproteins pass
transforming protein: tyrosine-specific protein.
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#formal_name Homo sapiens #common_name man,
30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#sequence_revision 30-Jun-1991.#
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CLASSIFICATION #superfamily human profein-typosine kinase at 1, profession kinase homology: SH2 Lomeofory: SH4 Lomeofory at ternative splicing: ATF; kinase-reducing atternative splicing: ATF; kinase-reducing transfer miles profein: phosphotranslerase
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                                                                                                                                                                                                         ##cross-references FlyBase:FBgn0000017
htrons 112/1; 130/1; 310/2; 449/1; 644/3; 735/1; 775/2; ...
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Best Local Similarity 47.5%: Pred. No. 1.246-16. Journally 15.20:
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##cross-references_GDB:119641; :M:M:164690
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Filipp A novel human generalicated to the abl proto-oncogene. Filips related to the abl proto-oncogene. Filips RNID:8705952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *! LLGVOTIE-PPPYJVTENMPYGNLELTLREGNREENTAVYLLYMATQINSAMBTI EKKN" ***
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30-jun-1991 #sequence_revision 30-Jun-1991 #foxt_change
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#domain SH3 howology #labol SH3\/
#domain SH2 howology #labol SH2\/
#domain protein kinase homology #labol Kin\/
#region protein kinase APP-binding motif
#length 1145 #molecular-Weight 124572 #checksum 3104
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##gross-roberences GB.M35295: NID:gl79492. FID:S178 92
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*product inner coat protein pil *status predicted *label
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 LLGVCTLE-PPFYIVTEYMPYGNLLDYLRECNREEVIAVVLLYMATGISSAMEYLEKRNF 4'F
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#domain protein Kinase humslogy Flabel KINN
#region protein Kinase AIP-binding motif
#length 1182 #molecular-weight 126342 #checksum 3637
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##residues 1-981 ##label RED
##residues 08:302009; NTD:q341887; PID:q331889
##rovs-references GB:302009; NTD:q341887; PID:q330 33A for the authors translated the cod3on 33A for the purpose translated the cod3on 33A for the codson 34A for th
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14-Nov-1983 #sequence_revision 09-Sep-1354 #558
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                                                                                                                                                                                             Score 890: Db 2: Length 1182:
Pred. No. 9.71e-151:
60; Mismatches 64: Indels
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PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
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Pred. No. 0.00e-00;
0: Mismatches 0: Indols (
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NACA S., PRADA M., MCAGLEY A., COOPER J.A., NAKAGAWA H.;
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AIP (BY SIMILABITY).
ATP (BY SIMILARITY).
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258; Conservative
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416 AA:
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BY SIMILARITY.
PHOSPHORYLATION (AUTHOR) (BY SIMILARITY).
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PROSITE: PS50002; SH3; 1.
TPANSFERASE. TYROSINE-PROTEIN KIMASH. All MINIMASH SH2 1- MA
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EUTHERIA, RODENILA,
-!- TISSUE SPECIFICITY: ENRICHED IN LYMPH-ID TISSUES.
-!- SIMILARITY: TO OTHER PROTEIN TYPOSINE MINASES IN THE DOMAIN BELONGS TO THE CSK SUBFAMILY.
-!- SIMILARITY: CONTAINS I SH2 DOMAIN.
-!- SIMILARITY: CONTAINS I SH3 DOMAIN.
-!- BMBL, X58631, G57508.
-!- PIR: S15094; S15094.
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Pred, No. 6,00e+00;
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ATP (BY SIMILARITY).
ALP (BY SIMILARITY).
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01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LASI SEQUENCE THIATE)
15-III-1998 (REL. 36, LASI ANNITATION UPPATE)
TYROSINE-PROTEIN KINASE CSK (EC 2.7,1:112) (***)
                                                                                   HSSP, P41240, ICSK.
PROSITE: PSO0107; PROTEIN_KINASE_AIP;
PROSITE: PSO0109; PROTEIN_KINASE_TYP;
PROSITE: PSS0011; PROTEIN_KINASE_TYP;
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201 209 AT
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314 BY
416 416 PH
450 AA; 50746 MW; H
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MEDLINE: 93096484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IISSUE-BRAIN;
                                                                                                                                                                                                                                              ACT_SITE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                       NF_BIND
BINDING
                                                                                                                                                                                                                                                                                                Scory Match
                                                                                                                                                                                              DOMAIN
DOMAIN
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                                                                                                                                                                                     DOMAIN.
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Thu Jan 14 13:43:16 1999

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PROTEIN KINASE.
AIE (BY SIMILARITY).
AIE (BI SIMILARITY).
BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                               EGI GEGYTVELENGGENTVERMANGSEVERENSKEASVEGGGGERKFSLØVLEAMEVLEGENNF 310
                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LIGVIVEBRO HALVIETMAN BRIVETLARBRANDECULKESLEVORAMERIEDNINE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                             311 VIRGLARARAVLUSELINVARUEESSLERAASI QOISKLI VKRTAREALAEKKISTKKSDVM 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 VERSLAARRINGVRETINGARVSEFSELKEASSIQLIGKLEVKWIAPEALKEKKFSIKSEVW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GALLUS GALLUS (CHICKEN).
EURARYGIA: MILAZOA: CHOKDAIA, VERIEBRAIA; IEIRARODA; AVES; MEGGMATHAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 SPGILLWEITSFORVFTFRIPLKIVVTFVLKSYRMDAPLGORFAVIDVKKNOSHLDAAIR 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 SFGILLWILIYSFGRVEYERIFLEUVIAVENSKRAKARARDASGEPAVEVAKNOWHLDAAAK 240
                                                                                                                                                                                                                                                                                                                                                                   o; Gaps
                                                                                                                                                                                                                                                                                                                                         Score 1840; DB 1; Length 450;
Pred. No. 0.00e+00;
2. Mismatches 3, Indeis c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P41239;
CHERR-1995 (REL. 31, CREMIED)
CLEPER-1995 (REL. 31, LASI SEQUENCE UPDAIE)
CLERCY 1995 (REL. 21, LASI ANNOLATION UPLAIE)
TYROSTNE PROTEIN KINASE USK (EC. 4.7.1.114) (C'SKC KINASE).
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2. Hismutches
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                                                                                                                                                                                                                                                                                                                        188 E1300
                                                                                                                                                                                                                                                                                                                                          guer, Match
Best Local Similarity 98.18;
Matches 253; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         431 PIFLQIREQLEHIKTHEL 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 PSFLQLREQLEHIKTHEL 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SALLIFORMES.
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DOMAIN
NP_BIND
BINDING
ACT_SITE
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121 VHPDLAAPNVLVSEDNVAKVSDFGLTFFASSTOGTSKLEVFKTAGEAFRFKESINSUTG 19
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P42679;
01-NOV-1995 (PEL: 32, CPEATED)
01-NOV-1995 (REL: 32, LAST SEQUENCE UPDATE)
15-77L-1998 (PEL: 36, LAST ANNOTATION UPDATE)
MEGAKAPYOCYTE-ASSOCIATED TYPSINF PEPTTEIN FINASE (ED LITTLILL)
(TUPOSINE-PEPTTEIN FINASE CYS, (HEMAIOPOIETIU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LLGVIVEEKOALYIVTEYMAKGSLVTVLESEVETTA DILLEESLLVDEAMEN DANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 SEGILLWEIYSEGRVPYPPIPLKDVVPPVEKGYKNDAPDGGFFAVYFNGKNONHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH2.
PROTEIN KINASE.
ATF (AY SIMILARITY).
ATF (BY SIMILARITY).
BY SIMILARITY).
FHGSPHFYLATIN (AULOS) (AT STVOMM. DF995EBC CROSE).
                                                                                                                                                                                                                                                                                                                                                      PIE: A41973; A41973.
PROSITE: PSOOLO; PROTEIN_KINASE_AIP: 1.
PROSITE: PSOOLO; PROTEIN_KINASE_AIP: 1.
PROSITE: PSOOLO: PROTEIN_KINASE_AIP: 1.
PROSITE: PSOOLO: SH3, 1.
PROSITE: PSOONOSE PROTEIN FINASE, AIF BINDING, SHI DUMAIN.
POMAIN
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MEDLINE: 94181267.
SAKANO S., IWAMA A., INAZAWA J., ARITAMA I., OHNO M., SUDA T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMO SAPIENS (HUMAN).
EUKARYOTA: METAGOA: CHORDATA VERTERRATA, 1EISAR-UCA: MAMMALIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NMKELKLLQTIGKGEFGDVMLGDYPGNKVAVFTFYDAIAGAFLAGAFTATA
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222
312
414
416
450 AA;
MEDIINE: 92196083
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MOD_PES
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PINDING
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DOMAIN
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Matches
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HAMANAHI I. IMAMA A. YAMAGUCHI N., SAKANN S., MATSUDA Y., SUDA I.,
N. HAMANAHI I. IMAMA A. YAMAGUCHI N., SAKANN S., MATSUDA Y., SUDA I.,
N. HINE G. A. T. C. A. (1964).
L. HINE G. A. T. C. A. SIGNITIONAL FOR THE SIGNAL INANGUOLION
S. HEMATOPPRETIC CELLS, MAY REGITATE TYPOSYNE KYMASL ACTIVITY OF
S. HAMILY MUNERAS IN HRAIN BY SPECIFICALLY PHOSPHCRYATING THEIR
FERMINAL MUNICATOR TYROSINE RESIDUE WHICH ACTS AS A NEGATIVE
HERMANAL MUNICATOR TYROSINE RESIDUE WHICH ACTS AS A NEGATIVE
HERMANAL SITE. II MAY PLAY AN INHIBITORY ROLE IN THE CONTROL OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ER - DG (IN REF. 1).
MISSING (IN REF. 1).
ARRIPPERLAEKLARELRSAGAPASV STLAMOSTSPINSON
P -> PAGHFYANWPESWPOSTAVOVPOFISGGRTPIVHLA
PKPGALTPPGGPWPQRTERVESAAWGH (IN REF. 1).
                                                                                                                                                                      DOTHED FATTAGEN.

NNELT BOTH FAMILIES STOUTANG SOUT NOWN BOT DENG BOT GRAPHER SOUT SAME COLD.

FRANK COLD. FEBRUARICAY, AVERARAM HOT.

FILL THEM. 249911068-1074(1994).
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SIMILARITY OF THE CATALOGY.
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ANALYTIC ATTACH N.
ANALYTIC ATTACH N.
FROTEIN TYROSINE FROSPHATE.
STROTE THE STROTE N. M. M. MICHASKI.
TINSTE SPECIFICITY: EXPRESSED IN VARIOUS XVELOID CELL LINES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ## SITES FAST 174 PROTECTION WITHARD ATE |
## SITES PROTECTION WROTHIN WITHARD BY 1 |
## SITES PROTECTION PROTECTION PROT
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                                                                                                                                                                                                                                                                                                                                                                                                                                       AVRANAM S. JIANTS. TA S. FT Y. DENG B. DOWLER WILL B. L. DOWLER WILL A AVENAM ... TO SEE OF 1842(1995).
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BY SIMILARITY.
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ATE (BY SIMILARITY)
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                                                                                                                            SSTE-MEDAKAPY - VTES:
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875147: GRAAC20; C
878144: GRAAC20; C
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GR46222
GR46222
GR46220
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875164) 384622?;
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S75154; GRO6220;
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                                                                                                                                                                                                                                                                                                                                                                     SECTION BORNEY.
                                                                              CHANGE THE REAL
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                                                                                                                                                                                                               THE NAME OF
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291 ILISVILHOTTGLYIVMEHVSKGNI VNFLRTRGRALVNITAGILLOFSTHVAF MEYTLESKKET (4)
                                                                                                                                                                                                                  349 VHPPLAAPNILVSEDLVAKVSDFGLAAAERAULDSSRLPVKWTAFFALKHRFTTSKRDVW 40R
                                                                                                                                                                                                                                                                                                                           409 SEGVILWEVESYGRAPYPKMSLKEVSEAVEKGYRMEHPEGTT-STVHVLMSSTWEAEFARE 40.00
231 NEOHLILGAOTGEGEFGAVLOGEVLOGEVLOGEVIRGEGTAGATELTGAVRAMGHRUVE ...
                                                                                                                                                            61 LLGVIVEEKGGLXIVTEYMAKGSLVDYLRSRGRSVLGGDFILLKESILDVGFAMEYLEGANNE ).
                                                                                                                                                                                                                                                    1 NMKELKLIOTIGKGEFGEVMIGPYFGHRVAVEGIKHRATAGAFTAEASVMIGJERISNIVE (C.
                                                                                                                                                                                                                                                                                                                                                             P41242;
01-FEB-1996 (REL. 31, CREATED)
01-FEB-1996 (REL. 31, LAST SEQUENCE SPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
MEGARANYOCYTE-ASSOCIATED TYROSINE-PROTEIN KINASE (F) 2.7.1.112)
(TYROSINE-PROTEIN KINASE CTK) (PROTEIN KINASE NTK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAIK OR CIK OR NIK,
MUS MUSCULUS (MOUSE).
EUKARYOTA, METAZOA, CHOFEATA; VERTEBRATA, THIRAPOGA: MAMMALLAS
EUTHFRIA: RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            **ALTERNATIVE PRODUCTS: BY ALTERNATIVE USAGE F Z INXINITY OF ACCEPTOR SITES, A SECOND, LESS ABUMINANT PROJUCT IS TO SIMILARITY TO OTHER PROFIEM TYPESSIME KINASES IN 181 TO SIMILARITY: CONTAINS I SHE CSK SHERAMILY.

**SIMILARITY: CONTAINS I SHE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHOW LIMIT. JARVIS C.D., HU G., NYE S.H., GERVAIS P. VEILLETTE A., MAIIS L.A., PROC. NAIL. ACAD. SCI. U.S.A. 91:4975-4979(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADAM D., CLASS K., FARGNOLL J., HOLEN J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROC. NAIL, ACAD, SCI. U.S.A. 91:2597-260;(1494).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BALB/C; TISSUE-THYMUS; MEDLINE; 94255451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 41-505 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                       469 PPFRKLAEKLAR 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 PSFLQUPEQLER 252
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KLAGES S., ADAM D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MATK_MOUSE
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NENGSCI, RES. 38:705-715(1994).

FURTION COULD FLAY A SIGNIALONI FOR IN THE SIGNAL TRANSDUCTION
OF HEMACOGCIL CELLS, MAY EGULARE IYROSINE KINASE ACTIVITY OF
SROTALITY MEMBERS IN BRAIN.
FROM THE ADP.
PROTEIN THROSINE PHOSPHARE.

STRONG THE SPECIFICATION CUICLES IN LARBHOUD ISSUES.

1 STRONG SPECIFICATION ENGINE IN LYMPHOLD ISSUES.

1 SINGLE ADP.
1 STRONG SPECIFICATION CONTRACTOR INVESTOR IN THE CATALYTIC

1 SINGLE ADP.
1 STRONG SPECIFICATION OF STRONG SIN THE CATALYTIC
 229 DIOHIIIGAQIREGEFFSAVEQSEYESLEVAVENIETINIAGAFIDEIAVMYKILHENIVE 188
 200 LECVILHH GINITHERNERGRIVERGERTRGFALVSISQLIQFALHVARGMENLESKKL 346
 61 LIGVIVEERGGENINTEENMANGSLUDYLESSPORSVLOODGILKESLEVOERMENLEGANF 120
 407 SPGVLLWEVESYGRAFFYFRYSTRYSEAVERSYRMEFFDGGFGSVHILMGSGWEAEPRAR 460
 347 VHRDLAARNILVSEDLVARVSEFSLAKAEFRSLLSSELLIVKWIAFEALKMGAFSSKSDVW 406
 18: SPGILLWEINSFREICHENDUNG FOR SERDER DER STELLT IN STELLE STELLEN.
18: SPGILLWEINSFREICHENDUNG SVERENDER DER ANNENVERWENDER DER AMMELDE AUG
 T MYKELKILQIIGKGEFGEVMLGEFFGNKVAVKCIKNDATAQAFLAEASVNIQLAHSNLVQ 60
 2; Gaps
 MEDLINE, 95105041.
KTO S.S., HORAN P., GRIFF J., ARMANINI M., PHILLIPS H.S., GOODARD A.
EMBL: D25738, G507290; -.
EMBL: D45243, S638659, ..
HOD. H31.92505. MAIN.
PRESILE: P800107; PROISIN_KINASE_AIP; 1.
PRESILE: P800101; PROISIN_KINASE_IPR: 1.
PRESILE: P850011; PROISIN_KINASE_IPR: 1.
PRESILE: P850001; SH2; 1.
PRESILE: P850002; SH2; 1.
TRANSTERNE: 1100011; FRILL: FRILL: KINASE, AIP-BINDING; SH1 DOMAIN; C1108 MAIN. PRESPUÉNTAILON, ALIENAILVE SPLICING; SH2 DOMAIN.
 CI-FEB-1995 (REL. SI, CREALED)
CI-FEB-1995 (REL. SI, LASI SEQUENCE UPDAID)
S-TT-100 (REL. SI, LASI SEQUENCE UPDAID)
MESARARICOTE-ASSOCIAL INFOSTORE PROTEIN FINASE (EC 2.7.1.112)
(TRECSINE PROJECT RELACED TO THE PROTEIN FINASE BATE).
 RAITUS NORVEGICUS (RAI).
EUVARYOTA, METAGOA, CHORDATA, VERIEBRATA: IELRAPOLA; MAMMALIA;
EUTHERIA; RODENIIA.
 FROTEIN KINASE.
AIP (BT SIMILAKITY).
AIP (BT SIMILAKITY).
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 very Match
est Local Similatity 57.9%; Pred No. 1.99e-245,
atches 146; Consernative 52; Mismatches 51, Indels 1
 SIRAIN-SPRAGUE-DAWLEY; IISSUE=HIPPOCAMPUS;
 00004-0000-E
00004-0000-E
0004-0000-E
0004-0000-E
0004-000-E
 SIANDARD,
 467 PPFRKIVEKLGR 478
 241 PSFLÇIREQLEH 252
 5.55 AA:
 SEÓUENCE FROM N.A
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NT_BIND
BINDING
ACI_SITE
 MATK_RAT
 SECTENCE
 Matches
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SEQUENCE OF 374-648 FPOM N.A.

MEDLINE: 84082064.

A CELL 35:333-401(1983).

-! CALAIVIC ACTIVITY: ATP - A PROTEIN INROSINE = ADP - FPOTEIN INFOSINE FINANCES IN INC. NATA (TO THE ABLIANCE) TO THE ABLIANCE IN INFOSINE FINANCE = SIMILARITY: CONTAINS I SH2 DOMAIN.

-! SHEL: M19690; G158600; JOINED.

R EMBL: M19691; G158600; JOINED.
 61 LLGVIVEEKGGLYIVTEYMAKGSLVDYLRSPGPSVLGGDCLLKFSLDVCEAMEYLEGNNF [2]
 308 VHPDLAARNILVSEDLVAKVSDFGLAKAELFRGLDSSFI,PVKWTAFEALFMGRFESSF,SDV 367
 368 WSFGVLLWEVFSYGRAPYPKMSLKEVSEAVEKGYRMEPPDSCPGPVHILMOSGWEAEPSR 427
 190 DEQHIILGAQIGESEFGAVLQGEYLGQKVAVKNIKCENTAQAFLEETAVMIKLQARALVA L40
 250 LLGVILHH--GLYIVMEHVSKGNLVNFLFTRGPAJVSTSÇILÇFALHVALGMEYLESKKL 300
 1 NMKELKLLQTIGKGEFGDVMLGDYPGNKVAVKCIKNDATAQAFLAEASVMTQLRHSWLVQ 6
 50; Indels 3: Gaps
 -!- SIMILARIIN: CONTROLL STATE | STATE
 Length 467:
 GERTLER F.B., HOFFMANN F.M.,
 SHO.
PPOTEIN KINASE
ALF (SY SIMILAKITY).
ALF (SH SIMILAKITY).
BY SIMILARITY).
 Score 1132, DB 1: L
Pred No. 3.490-241;
55; Mismatches 50;
 DROSOPHILA MELANOGASTER (FRUIT FLY).
ETKAPY-TA: META2OA: APTHPOPODA: INSECTA: IIITEFA
 21-JUL-1986 (REL. 01, CPEATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDAIE)
01-NOV-1995 (PEL 32, LAST ANNOTATION UPDAIE)
TYPOSINE-PROTEIN KINASE DASH/ABE (E) 2 1 112;
 PRT; 1520 AA.
-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN
 HENKEMEYER M.J., BENNETT P.L., GE
MOL. CELL. BIOL. 8:843-853(1988).
 7. 95 9 1.5
 Cuery Match
Rest Lonal Similarity 57.3%:
Matches 145; Conservative
 STANDARD;
 428 RPPFRKIVEKLGR 440
 240 PPSFLQLREQUER 252
 194
2000
2000
3000
311
467 AA.
 SEQUENCE FROM N.A.
MEDLINE: 88174728.
 DASH OF ABL-1
 ABL_DROME
P00522;
 ACT_SITE
SECTENCE
 DOMAIN
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8; Gaps 6;
 ATH (BY SIMILABITY).
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 447 (17WILEH-FFFY)]]EFMSHGNLDHTRSAGRETLDAVALLYMATGTASGMSKIESRNY 505
 THECHARPMELVERNKLYKVARFOLAKLARBOTYTARBOARFPIKWTAFBOLAVNKFSIK 565
 [4] VHPSTAABAYLASHTWAAKVSOFGLIR-- BASSTQOTG KLPVKWTAFDALFHEREFSIR 175
 594 STAWASTATIANTIATISMSEVENIOTITATHKOJKSTRAMERPPGCPPFVYOLJABUSKON 625
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 FIGURE (FEL. 32. CREATER)

-N V. 345 (FEL. 32. LAST SEQUENCE UPDATE)

-N V. 345 (FEL. 32. LAST SEQUENCE UPDATE)

-N V. 345 (FEL. 32. LAST ANNOTATION UPDATE)

-N V. 345 (FEL. 32. LAST AND AND AND AND AND AND AND AND AND ALLE.
 -1-SIXIIARITY: TO OTHER PROTEIN-TYROSINE KIMASES IN THE CATALYTIC PARIS, PERONS T. THE ARL STREAMILY.
T. SIXIIARITY: OTNIAINS T. SHE OWAIN.
T. SIXIIARITY: OTNIAINS T. SHE OWAIN.
 Scoro 943: DB :: Length 152::
Prod. No. 4.27e-194;
68: Mismatches 59: Indels (
 161836 MW; AE831F46 CRC32;
 PROTEIN KINASE.
 PRT: 1182 AA.
 VEZ IMMINISTRUMBUSHUN LA
 Conservative
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 STANDARDS
 1.2. AA:
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$100 0 # D
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F12684:
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 121 VHRDLAARNVLVSBDNVAKVSRPSLIK--HASS ICHTS KITVKWCAFFALERRRSSK (7)
 466 SDVWAFGVLLWEIATYGMSPYPGIDLSGVYFFLLFRGYFMR, FFGGTG-EVYELLER, WHWS (1.5)
 177 SDVWSPGTLIWEIYSFGRVPYPRIFIKBVVFRVEKSYKMIAFOGOPPAVYEVMKNAMHL, ...
 THROLMARNOT VGENHVVKVADFGLSPLMTGGTTTARA GAFFTAWTAFBSRAVMTESTR. 400
 347 LLGVOTLE-PPFYIVTEYMPYGNILLIYI PEONEHRUTAVULI YMATLISSAMHYLLIKKNI
 PROSITE: PSEGGO1: SH2: 1.—
PROSITE: PSEGGO2: SH3: 1.
PROSITE: PSEGGO2: SH3: 1.
PROSITE: PSEGGO2: SH3: 1.
PROSITE: PSEGGO2: SH3: 1.
PROSITE: PSEGGO3: SH3: 1.
PSEGGO3: SH3: PSEGG
 ABELSON MURINE LEUKEMIA VIRUS.
VIRIDAE: SS-RNA ENVELOPED VIRUSES: POSTITVE-STAND FELLE VIRITAE
ONCOVIRINAE.
 4 ELKLLOTIGKGEFGDVMLGDYRG-N-KVAVKOIKNDATA-GAFFADASVMTIJEH.
 NOCLEAR LOCALIZATION STONAL ()
 287 DITMKHKLGGGQYGEVYVGVWKKYSUTVAVKTLÆBUJMEVERHLKRAAVREL.
 Score 890: DB 1; Legark ''"
 Pred. No. 4.06e-181;
60; Mismatches 64; Hebel.
 ATP (BY SIMILARITY).
 40588722 CRC42;
 SEQUENCE FROM N.A.
MEDLINE: 83221648.
REDDY E.P., SMIH M.J., SRINIVASAN A.:
PROC. NAIL. ACAD. SCI. 0.S.A. HO:4428-4427(1944).
 REVISIONS TO 588-746.
REDDY E.P., SMITH M.J., SRINIVASAN A.;
PROC. NAIL, ACAD. SCI. U.S.A. 80:7472-7472(1944).
 PROTEIN KINASE.
 BY SIMILARITY
 PRT; 746 AA.
 PS00107; PROTEIN_KINASE_ATP; 1.
PS00109; PROTEIN_KINASE_TYR; 1.
PS500111; PROTEIN_KINASE_DOM; 1.
EMBL: M35296, G178993; --
MIM: 164690; --
MOSTIE: PSO0107; PROTEIN_KINASE_ATP
PROSITE: PSO0109; PROTEIN KINASE_TVE
 POLY-SER.
 7.17 - GLY
 PROCKICH.
 PC11.Y - P.RC
 1182 AA: 128343 MW.
 903
 Match
Lucal Similarity 48.28;
les 123; Conservative
 SECHENCE OF 233-327 FROM N.A.
 525 PADRPSFAETHQAFE 540
 STANDARD;
 237 AAMRPSFLOLREOLE 251
 660
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 288
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 ABL_MLVAB
P00521;
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US-08-955-841-3.rsp

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PDB; 1ABQ; 15-0CT-95.
 1123 AA:
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MEDILINE: 83245023.

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17.784 304154 140519.

18.784 141 304154 141 30514 30514 141 30514 141 30514 141 30514 141 30514 141 30514 141 30514 30514 141 30514 3
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6. LLOVINGERCOLNILTERMIRA SSLVETERSROBSVEST SILLER SILV VERMETERSKRF IIG
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 306 SOVWOLCH LABIALY DMERYROTH SIVYELLERDY BMERREGERKVYELMRACWOWN 365
 SOWWSPELLANDS ON THE TAXABLE SOWED THE TAXABLE DATE.
 127 CITHALALSSILAGGENISWANABLIVAVATIFESSINAVERIKEARANVERFRERANVERFRERING 288
 4 EDENILO DE PORTO DE PORTO DE PORTO DE LA TORIO DE PORTO 8, 3aps
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WANG CINCOL TELLEN BIL GUER BIL INDE BIL GRONER WILL BALTIMORE DIL
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 MOS MOSCOLOS (MIGSE).
EURARNIJA: MELAZDA: CHORDATA: VERTERRATA. TETRAPODA, MAMMALIA:
ETHERIA: RODENTIA.
 provy Match
Assistant Similarity 46.3%, Fred. Mo. 3.58c.177,
Marches i.e. Consentative (7, Mismatches 52, Indela
 MICH. CO. NO. COMORNODIA G. N. COMMENT CONTROL OF A VANTA
 TINGUE TEXTIS:

SPECIAL BENGGEST.

SPECIAL SECURE S.K., REDOY E.P.,

PRICE NATE AND ELL STORY E.P.,
 FSDRESFAEIHÇAFE 380
 237 AAMSTELLULKLUULL 251
 SECTENCE TROM N.A.
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 111 VHECLAARNYLVSEDNVAKVSDF511F--LASS-1Q11G-KLFVKKTAPEALPEKKFSTK 174
 420 SDVWAPGVLLWELAIYGMSPYPGIDLSQVYFLLEKDYFNBRPEGCPEKVYBLMRACWQWN 479
 61 LLGVIVEEKGGLYIVTEYMAKGSLVDYLRSRGRSVLGGD71LKFSLDVJEAMEYLEGNAF 1.
 ATE (PY SIMILARITY).
ATE (BY SIMILARITY).
AYENDERFURE TO PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
 301 LLGVCTRE-PPFYILTEFMIYGNLLDYLREGNRGEVSAVVLLYMATJISSAMETLIKKNET
 LT 12
ABL_HUMN
STANDARD; PPT: 1120 AA
POSIG: 91633:
POSIG: 916 (PRE. 01, CPEALED)
01-APP-1990 (PRI. 14, LAST SEQUENCE UPDATE)
11:-741-1999 (PRI. 36, LAST ANNOTATION UPDATE)
FROTO-ONCOGENE TYPOSINE-PPOTETN KINASE AB: (FT 2 7 1:12) (FIE.)
 4 ELKLLQTIGKGEFGDVMLGDYRG-N-KVAVKCIKNDAIA-QAFLAFASVMTCIFU.
 TRANSFERSE; TYPOSINE-PROTEIN FINASE PROTO-ONFOSENE: ALLERIN PHOSPHORYLATION, SH2 DOMAIN: SH3 DOMAIN: ALTERNATIVE SPICIONO-NUCLEAP PROTEIN; 3D-STRUCTURE, SH3.
 PROTEIN KINASE.
NYCIBAR LOCATIZATION SIGNAL (F
 Match Local Similarity 46.3%; Pred. No. 3.58e-177; etc. 118, Conservative 67; Mismatches 52; Indels
 241 DIIMKHKIGGGYGEVYESVWKKYSLIVAVKTLKERIMEVERT KEAANDA
 ಾಗೀತ್ರದ ೧೫೧೨ರು
 PRO-RICH.
 PROSITE: PSGC107; PROTEIN_KINASE_ATP; PROSITE: PSGC109; PROTEIN_KINASE_ITR; PROSITE; PSSGC011; PROTEIN_KINASE_DOM: PROSITE; PSSGC01; SH3; 1.
 12267£ MW.
 480 PSDRPSFAEIHQAFE 494
 237 AAMRPSFLOIREOLE 251
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 METLINI BEZTELZE
REPIN CL. HELSERKAMP N., REYMOLINS F.H. JR., STEPHENSON G.R.,
NATTHEE COLLEGE FOR CLUBER.
H.W. SAFLENS (HTMAN).
BTRAFY IA: METAZOA: CHCROATA: VERTEBRATA. TETBAPGEA: MAMMALIA.
BTIHBETA. PELMAIES.
 MELLINEL BY 284214
SHITVELMAN EL LIESHITZ BL. GALE R.P.L POE BLA GANDALLEL
Dell 4772777484 (1769).
 COMPTRM D.
 VERTINAL TO THE MAY BE HIGH KINS CORT. BALTIMORE DO COMBORN DO MOTO NATAL ACAD. SOLUTISTA 89101673-11677(1992).
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 6 G. V.
 FUNERAL V.O. ZHENG J., OVERDOIN M., MAYER B.C., COMBORN D., STRITTIPE RICKET PRACT (1995).
 NAM BOLL BASHS W. L. ROBERTS I.M. PRECERING C.A., SIECT BE 41.15-III4(1995).
 TOURD TO
 CONTRACTOR WORKLING OF SET DOMAIN, MEDITING GST-429, STREAM LLL WADE R.C.: FF TEINS DIEZETT(1944).
 FINS THE MAYER BLOW BALLINGER D
 PAINSTEIN BL. MARGELLE C., ROSNER A., CANAANT E. LERAZIN J., SHITH S.L., TROBE C.M.;
 X-RAY HYSTALL GRAPHRY (2.5 ANGSTROMS) OF 57-218.
 Benigalze.
V Poli Elival Mood Kkel Boo Marcelle
 WHITEN I
 98/3 INEL 94142/31,
IN KT181 KL. FOIAKI M., DAN F.,
IEUKEMIA 8:343/3/344(1994),
 SIRTITIBE BY NMR OF SHE DOMAIN.
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 SELTENTE F ROL-426 FROM N.A.
 SECTENTE OF 825-845 PROM N.A.
 E E.F. (ZANANI) E.:
PURINE 4:1477-1481(1989).
 SECTION OF ZTOGG FROM N.A. METGLINES BROKSSER.
 :697-704(1992).
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MALE FIRE CANADA
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 BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
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 PROTEIN KINASE,
NUCLEAR FORALIZATION STONAL (BUJENLIAL)
 241 DITMKHKLGGCQVGEVYEGVWKKVALTVAVA (1 kfolyhyddio y fylywfei (ynenemio) 🧓
 BREAKPOINT FOR TRANSLOVATION FOR FM
 Ouery Match
Hest Local Similarity 46.39; Pred. No. 6.43e-177;
Matches 118; Conservative 65; Mismatolos 67; Indo.8 95
 360 THRDLAARNOLVGENHLVKVADFGLSRLMTGDTYTAHAGARFTERKTALESTANN
 LLGVCTRE-PPFYI ITEFWITGNI PPH HENROHWAVVILFFALL
 61 LLGVIVEEKGGLYIVTEYMAKGSIVDYLHERGENGSTGRESSGLV VERSE
 L > P (IN PEF, 2)

AF > S (IN REF, 2)

L Y R (IN REF, 2)

F Y R (IN REF, 2)

S > T (IN REF, 2)

A Y (IN REF, 2)

E Y Y (IN REF, 2)

E Y Y (IN REF, 2)

G Y F (IN REF, 2)

G Y F (IN REF, 2)

G Y F (IN REF, 2)

SPS - RPG (IN PEF, 2)

SPS - RPG (IN REF, 2)

RI - S (IN REF, 2)
 (BY SIMILARITY).
 122944 MW: 14PC7714 CRC323
 BCR-ABL ONCOGENE.
 PROSITE: PSO0107; PROTEIN_KINASE_ATP, PROSITE; PSO0109; PROTEIN_KINASE_TR, PROSITE; PSSO011; PROTEIN_KINASE_DOM, PROSITE: PSSO001; SH2; 1.
PIF: A25582; TVHUA,
PDR: 1A82: 31-JAN-94,
PDB: 1ABL; 01-NNY-94,
PDR: 2ARL; 04-6EP-97,
PIH: 1AWC; 28-JAN-98,
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 !!! RHFIHROLAARNCLYSSHNIVKTADFSLARFUKEDIYTAHAGAKFPIKWIAPEGLAFNIF 470
 118 NASTABLIANDAN SEEDAWARYSEEGIT - KERSSEGDIG-KLPVKRTAPEALPFKKF 173
 352 LVRILGVOTNI ACTULITERNONDLEHIEREPRESTUPPITLVQMASQIASGMSYLBA 410
 SE LYCLLGVIVEERGGLYIVTEYMAKGSEVOYLRSRGYLGGDCLLKFSLDVCEAMEYLEG 117
 292 DRESTINSHRING FRANKE HATTIAVEALKEDAMPLHEFLADAATMEDLHEKN 351
 I NAKODEDLI DESEESTIVETITE FINE FVANKOIRNDAIA-QAFIAEASVATQIFHSN 57
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accivs 120: Conservative
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C --- DEVELORMENTAL CONTAINS 1 SH2 DOMAIN.
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C --- SIMILARIN: CONTAINS 1 SH3 DOMAIN.
C --- SIMILARIN: TO CONTAINS 1 SH3 DOMAIN.
C --- SIMILARIN: TO CONTAINS 1 SH3 DOMAIN.
C --- DOMAIN: BELLONGS TO THE BIK SUBFAMILY.
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DR EMBL: M22051: B1934; ALITERM.
DR PIR: A23051: A22051.
DR PIR: A23051: A22051.
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DR ROSIEL FS0002: SH3: 1.
DR ROSIEL FS00015: SH3: 1.
DR ROSIEL PS00015: SH3: 1.
DR ROSIEL PS00
 TILL MATSWORTH S.B.:
 4 ELKLLQTIGKGEFGDVMLGDYRGN-KVAVKCIKNDATAQA-FLAEASVMT.LFH
 329 QIMIMEELGSSQFGVVRRGKWRGSIDTAVKMMKEGTNSEDDFIEEAKVMTKL.
 Length 59
 73: Indels
 PHOSPHOPYLATION (AUTO-)
S -> F (IN Fit L).
 WADSWORTH S.C., MADHAVAN K., EILUDEAU-WENIWURTH D.:
NUCLEIC ACIDS RES. 13:2153-2170(1985).
 PROJEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILAKITY).
BY SIMILARITY.
 SOLI 14
PRIZECTORE STANDARD, PRI: 590 AA.
PRESCRIPTION PRISE.
01-AUG-1968 (REL. 08, LASI SEQUENCE UPDAIR)
01-AUG-1997 (REL. 35, LASI SEQUENCE UPDAIR)
01-AUG-1997 (REL. 35, LASI ANNOTATION UPDAIR)
1YEOSINE-PROTEIN KINASE SRC260 (EC 2 7.1 112).
BRICAGA OF SPC29 A P SPC2.
BRICAGA OF SPC29 A P SPC2.
BRICAGA OF SPC3A AND SPC3.
BRICAGA OF SPC3A AND SPC3A BRICAGA BRICA
 ; DB 1; L6
5.90e-175;
 66; Mismatches
 MEDLINE, 87257924,
GRESURY P. J. KAMMERMEYER K.L., VINCENT W.S.
MOL, CELL, BIOL, 7:2119-2127(1997),
 45.6%; Score 865;
531 NWSPSDRPRFRDIHFNLENLISSNSL 556
 234 HIDAAMEPSEDQIREQIEH-IKIHEL 188
 65887 MW.
 SIMILARITY WITH BIK SUBFAMILY.
 SEQUENCE OF 356-484 FROM N.A.
 Lucal Similarity 43.5%;
es 114; Conservative
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64 FRUIVDERGER FRIVTERMARGSLVDYLRSROFSVERR-DOLLKFSLDVOEAMEYLEGINF 126
 444 HHEELAARWIIVSSENVVKVADEGLARYVLDDOYTSSGOTKEPIKWAPPEVLNYTREGSK 507
 121 VHRDLAARNVLVSEDKVAKVSDFGLTK---EASSTODTG-KLPVKWTAPEALREKKFBTK 176
 For STAWAYGVIAMGIIFICGAAAPGRIKNTEVVERVQRGIIIEKPKSCAKEIYDVMKLCWSHG 567
 177 SAVESFOLDARDIYSFORVPYPRIPLKDVVPRVFKGYKMDAPDGCPPARVEYERMONHED 236
 |- HIS PROTEIN IS SYNTHESIZED AS A GAC-ARL POL POLVPRITEIN, STATE L TV YT PET PEPYTITEFMIYGNDLDYLRBÜNROEVNAVVLLYMATQISSAMEYLEKKNF 308
 4. LIGVIVEEROGLYIVEEYMAKGSLVDYLERRORSVLOGDYLLKFSLOVJEAMEYLEGNNF 120
 4 ELKLIGITIGKGEFGTVMLGEVRS-N-KVAVKCIKNDATA-OAFLAEASVMTGLRHSNLVQ 60
 * * THECTAAFWILVBENHLVKVAUFSLSBLMTSUTYTAHAGTKFPIKWTAFESLAVNKFSIK 368
 THE STAWAR WILMRIA (YOMSPYPOIDESQVYRILLEKOYRMERPBGCPEKVYRI MRADMOWN 428
 17 STVWSF HILLMELTESFORVPYPHIPLKDVVPRVEKGYKMIAPDGCPPAVYEVMKNOWHID 236
 INE SAROMA VIERS (STRAIN HAMDY-ZUCKERMAN 2).
CLAE: SS-RNA ENVEL PET VIRUSES: POSITIVE-SERAND: HETR VIRIDAE;
 THE SIME FERTHERN KINASH FRANSFRENING PROTEIN ABL (EC 2.7.1.112).
 FRWAN 1. SILVERINE A. D'ANDREA E. SNYDER H.W. JE. VIT C. A. DIADER H.W. JE. VIT C. A. SILVERINE A. NGTVEN H. HESMER P.; VIT C. A. SILVERINE A. D. SILVERINE A. MENTEL A. HESMER P.; VIT C. A. SILVERINE A. PROTEIN TYROSINE - ADP.
 PERTER ESCOND SHEET FROM TRANSFERMENT TROSINE-PROTEIN KINASE. HANNEHEARED UNCOUNED SHE DOMAIN; SHE DOMAIN.
 45.4%; Score 862; DR 1; Length 439; 45.2%; Pred. No. 3.230.174; defect 65; Mismatches 62; Indels
 62) Indels
 PRI: 439 AA.
 439 AA7 50004 MW: B2320852 GRC32;
 SH2.
PROTEIN KINASE.
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 -27 AAMBESFLULARQUEHIKTHEL 258
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Search completed: Wed Jan 13 12 16.58 1999

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4 556-153
7 866-153
7 866-153
7 966-153
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1.11e-146
1.69e-145
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725.044 Million cell uprates/sec
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(1-258) from TS08955941.pep
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1 WHKELKLOTIGKGEFGDVM......MRPSFLOLREGISHTKTHE 258
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 3.1 VHRDLAARNVLVSEENIAKVSDFGLIKEASAIQDISKLFVRMIAFEALREKLFSIKSDVW 37.
 231 LLGVIVEDKSGLFIVTEFMAKGSLVDTLASKORSVLOGEGLIVFSLDVSEGMEYLESNNF ''.
 51 LLGVIVEEKGGLXIVIETMAKGSLVDYLPSP9FSVLGGDCLIKFSLDVOLAMEN LEGNNF 12.
 1.1 VHPDLAARNVLVSEDNVAKVSDFGLIKEASSTQDIGKLPVKWIAFLALKERKESIFSDVW 18.
 191 KMRDLKLOHIIGKGEFGDVMLGEHOGVKVAVKCIKNDAIAQAFTAEANVWTGTGHKNLV
 XENOPUS LAEVIS (AFRICAN CLAMED FROG).
EUKARYOIA: METAZOA: CHORDAIA: VERIEBRAIA: IETRAPOLA: AMPHIBIA: ANTBA:
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(SCHMIDT-RUPPIN D STRA
 y Match 87.4%; Score 1559; DE 13; Length: 45 Local Similarity 83.3%; Fred. No. 0.06-00; nes 215; Comservative 28; Mismatches 15; Indels
 PSSEIM.
FER (FHS/FPS PFLATFD)
SRC.
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MURCHY S.M. MORGAN D.O.:
MURCHY S.M. MORGAN D.O.:
SUBMITTED (MAR.1998) 12857840: -.
EMBL. AF052430: G2967840: -.
FOREL AF052430: A2967840: -.
FOREL AF052430: G2967840: -.
 01-AUG-1998 (TREMBLREL: 07, CREATED)
01-AUG-1998 (TREMBLREL: 07, LASI SEQUENCE UPDAIE)
01-AUG-1998 (TREMBLREL: 07, LASI ANNOIATION UPDATE)
 450 AA.
 PRI;
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 HIRAC A., HASHIYAMA M.,
 189 NUSHLILISAGIGEGEFFGAVLUGEFLGOFVANKKIKGEVTAGAFLUEIAVEIKLOHKKLVK 248
 AMATON 60.5%: Score 1.49; UB 11; Length 465; Longth Similarity 57.5%: Pred No. 2.736-227; Conservative 53; Mismatches 51; Indels 2; Gaps
 24.4 IISVIIHH--GLYIVMEHVEKOHLVNHTAIKAKALVSISGLLOFALHVAESMEYLESKKL 306
 () INVIVERENCELYIVIERWAKSELVERERRERENEGSDOLLKFSLDVOFAMETISGNWF 120
 *.7 VHROLAARNILVSPYYVARVERFOLARAERKGLDSSRLPVKWTAPEALKNGRESSKSDVW 366
 12.1 VHPCLAACHWI VAR AVARANCOFOLITRDASSTUDI ÖKLI VKMFAPFAT FORREGIRGEVW 180
 *** SETVIIMENESYGRAPYPPMSI.KEVSEAVDKÖYRMEPPDGCPGSVHTIMGSCWEAEPARR 426
 : NAKIIIKI ETIIRGEEGOVMIIIDERGARVEEKKIKATALAJARLAEASVMIJIRRENLVO 69
 141 SPULLMELYSRURVPRYPRIPLKYVVPRYPRYPRYDATCAFFAVLEVMKMUMHLDAAMR 240
 HYLL TYPOSINE (INASE.
HYLLE
HYLLE
MOS MUSCULUS (MOUSE),
BIRAHYOTA: METAZOA: CHORDATA: VERIEBRATA: TETRAPODA: MAMMALIA;
EUTHERTA: ROTENIA.
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HTS NISTIDES (MOGSE).
HTSABYOTAL MENZOAL CHORDATAL VERTERRATAL IETRAPODAL MAMMALLA.
HTHELAL ROLENICA.
 SHITEN'E SHIZEN'A. MEN'A. MEN'EN'E SHIZEN'A. MEN'EN'E A'V. PELIAVEKII A.V. VISSHI T.V.
 G. GREATED.
12 GART BROTEBOR TOWNER,
26 GART RESOURTION CHORSES,
 ALIMAN STILL SHIMA FOR STILL STATES (1998).
HI PHISE RES. CORMIN. 221(172(179(1998)).
HI PHISE RES. THE PROPERTY KINASE_AFF. 1.
HENCE PROBLEG PROPERTY KINASE_TYR: 1.
HENCE PROBLEG PROBLEG. MINASE_TYR: 1.
HENCE PROBLEG: PRIBASE.
SHIPLY B. JOHNAN, STETI MM. FEUSTRED CHORS.
 "N.V. 1.446 (TREMBLER) OJ CREATED)
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STRANM 12A N. CHIPELZO: TISSCE-EMBRYONIO STEW.
 F. K. AKAL MATK 305,673-503(1994).
F. KILL ST473: 0457264.
F. F. SIER ST573: PROTEIN_KINASE_APP 1.
F. SIER PSC 17: PROTEIN_KINASE_APP 1.
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 1 NMKELKILQTIGKGEFGDVMLGDYRGNKVAVKCIKNDATAQAFLAFASVMTOLKHSNLV
 414 SFGVLLWQVFSYGRAPYPKMSLKEVSEAVEKGYRMEPPINGCPGSVHILMISGWEAFFARF 411.
 181 SFGILLWEITSFGPVPYPRIPLKDVVPRVERGTRMIAPHACHTAVYEVMKNIWHLIAAMH
 190 MIGHUTLSAQIGESEFGAVLQGFFI LLF VERIE HVTALAHTTELAVUKKULHENIVE LIT
 Owery Match
Best Local Similarity 56.7%; Pred. No. 1.440-23;
Matches 143; Conservative 53; Mismatches 54; Indels 3; Sajs 1545.
 367 SEGVLLWEVESYGRAPYPKMSLKEVSEAVERRYRMEPPEGCPOTVIVITYLMSSCWEDE (7.6.)
 307 VHPPLAAPNTIVSEELVAKVSDEGLAKAFAKGLINSKLPVKWTALEALKEEAE ...e
 DOMO SAPIENS (HUMAN).
BUKABYOIA: METAZOA. CHOPEATA: VENTENBAIA: TETHAHETA: INDUNCE
ETHERPIA: PRIMATES.
 249 LLGVILDO--GLYIVMEHVSKGNLVNFLKTRGRALVNTAQLILLFSERVEL DE-
 01-000-1996 (TREMBLREL 01, CHEATED)
01-000-1996 (TREMBLREL 01, LAST SEGGENCE THIAIF)
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 P.K.:
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 427 PFFRKLAEKLAR 438
 241 PSFLQLPEGLEH 252
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12: VERGLAARKIIVSELKVARVAEBOLIK ** ETTI 13 ** EVVVVI AREA ** ETTI 15 ** EVVVVI AREA FEKKESIK 176
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 CONTRACTOUS AND EMPLOYED VIROSES, ELETTIVE STRAME, RETRUVERENCE.
NOTVERNAE.
 ABO.
BON' SABIDNS (HOMAN).
F"KARROIM, METABOA, CHORDAIM, VERIEBBAIM, TETRABODA, MAKMALIA.
 Per, March. 46.0%. Score 874. DB 14. Length 281. ost focal Similarity 46.3%. Pred. No. 2.356-171. date: 10.3.2.3.3. date: 67. Mixmatches 62. Indels
 PRELIMINARY, PRE, 981 AA.

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 237 AAMRPSEICIRECLE 251
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 SECUENCE FROM N.A.
TISSUE-LONG CARLENDAM.
MEDILINE: 9554474.
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MEDILINE, 84066136.
HEISTERKAMP N., STEPHENSON J.R., GROFFEN J., HANSEN P.F., KLEIN A.,
RAPTPAM C.P., GPOSVELD G ?
 SIQUENCE FROM N.A.
ILSGUELLUNG CARCINOMA:
MEDLINE: 90016849.
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TISSTELING CAPCINOMA,
MIDILINE: 812440544
HEISIERRAMP N., STAM K., GROFFEN J. DF KLEIN A., GROSVELD G.,
NATUPE: 315-758-751(1985)
 SECTENCE FROM M.A.
TISSUE-LUNG CARCINOMA:
MEDITHES REDSBY7.
EERWARDS A. PURTH C.M., WESTREONE C.A., FASKIND M., BALLIMINE MORE OFFILE O
 MEDLINE; 82199444.
GROFFEN J., HEISTERKAMP N., GROSVELD F., DE VEN W., STRHRENS
SCIENCE 216:1136-1138(1982).
 TISSUE=LUNG CARCINOMA;
MEDLINE: 90082420.
FAINSTEIN E., EINAT M., GOKKEL E., MARCELLE C., CROCE C.M..
 ANDPEWS D.F., TOMPKINS C.K., HENDFICKSON S.L., SINGER J.K. ONCOGENE 5:441-444(1990).
 TISSUE-LUNG CARCINOMA;
MEDLING: 9702819.
SHIVVELMM: 8- ILFSHIZ B., GALE K.P., R.E B.A., CANAAN:
CELL 47127-284(1986).
 CRUFFEN CL
 SEQUENCE FROM N.A.
IISSEE-LING CRECINOMA;
MEDILING SE20029.
LIFSHITZ B., GALE R.P., CANAANI NAIURE 315:550-554(1985).
 IISSUE-LUNG CARCINOMA:
MEDLINE: 83187991
HEISTERFAMP N , GROFFEN J., STEPHENSON J.R.;
 SECTENCE FROM N.A.
IISBUE-LUNG CARCINOMA;
MEDILNE; 87064346.
FRIVELT 3, VFWCEF I., VAN ACHEVYEN I., I.
BAMACHANPAN K.L., HEISTERKAMP N., STAM K.,
MOL. CELL. BIOL. 6:607-616(1986).
 TIPIT ACIDS PES. 10:459-472(1980).
 MOL. APPL, GENET, 2:57-68(1983).
 SEQUENCE OF 1001-1130 FPOM N.A.
 ONCOGENE 4:1477-1481(1989)
 WATUFE 206:239-242(1983)
 TISSUE-LUNG CARCINOMA;
MEDLINE; 90191734.
 TISSUE=LUNG CARCINOMA;
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 FISSUE=LUNG CARCINOMA;
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 S EFFICANT COURSEMENT OF HORESCOOT COUNTRY MORET MOUNTEDWISEN TO VAN BAAL GOUR HAGEMILDER AND GROSVELD GOD
 4 FIREIGNINKSEPONVKLOPVROENSENSENSKROTRKNOMINGABLABASVKTILKASKLVU 69
 TONCOGENE ATP-PINDING.
 OF KLEIN A.
 DR 4: Length 1130;
 TOPENHAVER C.M., BRUNNING R.L.:
 Mismatches 63; Indeis
 STRMITTED (WAR-1--1) TO PROFITE DESCRIPTOR LAIN BANKS.
PRINCIPO 207564: 0514267; -...
PRINCIPO PROFITOR PROTEIN_KINASE_ATP: 1.
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 THESTS (1994), PRIVERSITA OF OKLAHOMA,
 Score 873;
SHIPM THE PROME NATAL
LISSTH CITYLE CARCINGMA,
MICHIGAN, 441 1982.
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 SELTEN TE BERNANA.
138STELTEN OARDINOMA.
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138. LELL MOLTER U.S., PORTER U.S
 . 2222.
 Local Similarity 46.3%;
 STUDENTS TROM N.A.
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ATOS V. B.L. LIPMAN 1.C.
 SELTENTE FROM N.A.
TISSTELLING CARCINGMA:
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7811. 36:93-94 (1984).
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MEDLINE: 95394474.
CHISSOE S.L., BODENTEICH A., WANG Y., CIAN E., FURIAN S., CARBIREE J.S., FREEMAN A., HAMFO C. S.T.ATET H. FOR H., FOR H. S., GROFFEN J., HEISTERKAMP N., POE H.A., GENOMICS 27:67-82(1995).
 420 SDVWAFGVLLWEIATYGMSPYPGTDI SQVYPT LEKDYRHDRFRAGE ENVIDDARA TALLA
 177 SDVWSPGILLWBIYSPGRVPVPPIILKIVVFWFFFWKRAFIGATTGAVFFVRZETWEE
 HANCEN LAIL REFINAL
 360 THEOLAARNOLVGENHLVKVAEFGLSRUHTGEFTTAGA ÄKETTKWIALESLATURE.
 GROSVELD F . DE VEN W. STEPHENSEN
 TISSUE-LING CARCINOMA:
MEDLINE: 88038877,
RPRNARDS A., RURIN C.M., WESTBROOK of A. FASKING M., PALITHOLO MOL. CELL. BIOL. 7:3231-3236 (1947).
 EUKARYOTA, METAZOA: GHOPPATA: VEKTEBKATA: TETRAPOTA: KAMMALTA;
BUTHERIA: PRIMATES.
 SHIVELMAN E., LIFSHITZ B., GALE R.P., POE B.A., CANAAN:
CELL 47:277-284(1986).
 01-NOV-1996 (TREMBLREL. 01, CHEATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNUTATION UPDATE)
 MEDLINE: 87064346.
GROSVELD G., VERWORRD T., VAN AGTHOVEN T., DE KLEIN /
RAMACHANDRAN K.L., HEIGTERKAMP N., STAM K., OBOPPEN /
MOL. GELL. RIOL. 6:607-616(1986).
 PRT: 1149 AA
 HEISTERKAMP N., STEPHENSON J.H., GROFFFN : BARTRAM C.R., GROSVELD G.,
 STEPHENSON J.R.;
 PROTO-ONCOGENE TYPOSINE-PROTEIN KINASE.
 HEISTERKAMP N., GROFFEN J., STEPHEN J. MOL. APPL GENET. 2:57-68(1983)
 GROFFEN J., HEISTERKAMP N
SCIENCE 216-1138(1982).
 480 PSDRPSFAEIHQAFE 494
 PRELIMINARY;
 237 AAMRPSFLOLREOLE 251
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 SECUENCE FROM N.A.
TISSUE-LUNG CARCINOMA;
MEDLINE: 9539474.
 SEQUENCE FROM N.A.
TISSUE=LHNG CARCINOMA;
MEDLINE: 82199444.
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TISSUE-LUNG CARCINOMA;
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MEDLINE; 83187991.
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BILSELWERGE N. SERM AL. GRUBEEN CL. DE KIEIN AL. GRIEVELL.
NATURE HISTORE-761(1985).
 VN. 6. M. G. G. G. CHIERLING COROL. HENCESCONCY SOLD, SINGER CONT. NOCOSENE SIA41-444 (1990).
 SECTENCE FROM N.A.
IISSTE-LING GARDINIMA:
IISSTE-LING GARDINIMA:
RESEN SELVE SOURCE DE CARRED DE LARREN C.T.
NOCHIC ALLOS NES. 177561 7542(1989).
 SELUENCE FROM N.A.
TISSUE-LUNG CARCINCMA:
MECLINE 922UST,
TITE OFFICE OFFICE C.M., BRUNING R.D.;
BLUCE RIJEGT-1572(1993).
 ALC: ALC
 SECTENTI TROM N.A.
TISSER-LUNG OBSTRUMAN,
TATUS, W. LIPWAN D.C.:
STRN:THE (JOL:1994, I: EMEL)SEMERATED INTA BANKS
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 ATRIANNA DI MANDENDEBEN JI, HONFELDOT LI.
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LETREMIA (1997-122(1990).
 HESIS (1494), TNEVERSITY OF ORLANDMA
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TISSUE-LING DATAININA,
MEDILINE: 85240529,
MAIDAN BL. (DESHIE S., DALE R.E.,
MAIDAN, SII. (SII. (SEC.))
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TISSTE-1000 TARTINTMA:
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MEDILINE, 90182421.
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MAGLINE: 90141734.
 (ASAT)1851-14115 GNESCON
 EMBE: 007563; G514268; -.
 SECTENDE FROM N.A.
TISSUESCONO CARCING.
R.M. R.A..
S.EWILLE (MAR. 1974) T.
 SELCENCE CROM N.A.
TISSUR-LONG CARCINOMA,
MIDINE, 90.94679,
FURNAMAN D., YAN DONDE
 SECCENCE TATALATA
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 4 FIRELDIIGRGEBESOWESDYRS-N-RVAVROIRMIATA-GATGARASWHOGHRUNDUR
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 61 LIGVIVEEKGGLYIVTEYMAKGSLVDYLRSRGRSVLGGDGLLKFSLLVTRAMFYTF TO
 379 IMPOLAAPNOLVGENHLVKVADPGLSPLMTGDIYTAHASAKEPIKWIASSAAAA
 Length 1145
 Query Match 45.7%; Shopp AFT: Toppth F98: Best Local Similarity 43.7%; Pred. No. 1.09e-169: Matchus III; Conservative Ff. Mishui Acs 73; Indels
 SEQUENCE FROM N.A.

GUARNIERI D.J., DODSON G.S., SIMON M.A.;
STRATTER (JAN-1998) TO EMBL/JENRANK/UDEJ DATA BANKS.

SEREL, AFO44337, G2827464; -.

SEQUENCE 588 AA; 65234 MW; 8F552080 CRC32;
 245032 PPELIMINARY, PRI; 588 AA. 045032 0045032. 001-00W-1998 (TREMELREL 06, CREATED) 01-10W-1998 (TREMELREL 06, LASI SEGMENTE "PLATE) 01-10W-1998 (TREMELREL 07, LASI SEGMENTE "PLATE) 01-AMM-1998 (TREMELREL 07, LASI SEGMENTE)
 Query Match
46.0%; Score 873: DB 4: Le
Best Local Similarity 46.3%; Fred. No. 4.06e-171:
Mitches 119; Conservative 66 Mignations 67
 DEGGERATIA MELANGGASTER (FRUIT FIY).
BUKARYOTA, METAZOA, APTHROPODA, INSECTA: DIPTERA
EMBL: 007561: G514268; JOINED.
PPOSITE: P600107: PPOIBIN_KINASE_AIP: 1.
PROSITE: P800109; PROIBIN_KINASE_IYR: 1.
PPAM: PP0017; SH2.
PPAM: PP00018; SH3.
 499 PSDRPSFAEIHQAFE 513
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 144 DEGET SKRIKE-IVIVIEVMKROSLINVLRKRERZILIORRGILDEMOTIVSKRETYLERRN 444
 61 LAYIVEEN KAIVIVTEYMAKGSLVDYLRSRGRSVLGG-DCLLKFSLDVCEAMEYLEGNN 119
 445 VIRBULAABUULVISENVVKVAOPELABEVLEDEN JOSA HIKKKAUPUL HUTRIGG 504
 12" FVERTIAARNVIVSEDNVAKVSRESIIK - EASSTODIS-KLPVKWIADEALEEKKES! 176
 FUS KSBUWAYBULHANKHILHANKMEYBELAKHILUVERVOKSIILLEKPRSCAMELYDUMKLOWSH 564
 (74 KSIAWSPGILIWETYSPIBATFYPPRIPILKBAVPRAEKÄY+MEAFESGPIFAVTEVBKMEMEL 235
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 13.4. tempth 37r; Score 862: DB 11: Length 37r; Tis Similarity 51.8%; Pred. No. 1.69e-168; Tis: Conservative 50: Mismatches 54: Indels 6: Gaps
 LOG LATTHLITTAHADAKOOLUMTAPIBLAYNTESIKSLVWAEGVILWELAIYSHSPYPGIDLS IRG
 ** TRETSHEEVTAVOLINMATULSSAMENLEFFRANTERCONARNOLVOENSY KVAUTOLSE 24
 11 - BASS-TOTES-KITVER ABERTREESTRACVESEGILLWEITSFORVEYPRIPLE 203
 * VAVE ... AND THE FEAR AWARTERS HANDLESS TELEF PREVIVIEW BY GALLEY 64
 ** VAVETTENLAFA - AFLABANAMTOLRHSNINDILLSVIVBERGGLYIVTEYAAKSSLVDY 87
 ARA,
MYS MYSTHUS (MICSE),
FYKAPY YAS MITAPOA, THOROATA VPRIBERAIA, THIRAPOAS MARKALIA;
 VYTTIER IVERELFECTITIVIELMEAVWKWSPADRPSFAETHQAFE 232
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FRI: 512 AA.

PRELIMINARY,

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248 TKLVEPLGARGEPSEVMMGYYNGHTKVAVKSFKGGSMSPPARFFAPRIFMFUFLURGELVRELY - 0 11
 308 AVVIOE--PIYIITEXMENGSLVDFFKTPSSTYTTINKLLDMAAGTABSWYFTERBNYTH 👵
 63 GVIVEERGGLYIVTEYMAKGSLVDYLARGRSVLAPHOLLKESTLVPFAMHYLESHANHYLE.
 y. 17:
 426 VWSFOILGTETVTHSPIPYPSMTWIRVIGWILAGVFMVERON THEIXLIMHITMFFFF
 366 RDIPAANILVSDTLSGKIADFSLARLHDBIVTAARSTAKI FIRKITARDAIN KATETIRSI
 123 RDLAARNVLVSEDNVAKVSDFGLTK - BAGS I GOTORGEVKWITABBALBEKKISTERS
 XENODUS LAEVIS (AFPICAN CLAWED 1103);
FURABNOJA: MEJAZOA, CHORDATA: VIRTERRATA: TETRAROGA: AMBERMAN, AN
EUKAPYOTA: METADOA, CHOPDATA: VEKTEBRATA: TETRAPODA: MAMMALLA:
EUTHERIA: PRIMATES.
 / Match
Local Similarity 45.1%; Score 814: DB 4: Lynath 5:2:
Local Similarity 45.1%; Pred. No. 4.26e-157;
Local Similarity 45.1%; Pred. No. 4.26e-157;
Local Similarity 64: Mismatches 68: Linkels P.;
 223 TRMVERESAGGEGEVMMGETNNSTAVAVRTTE POTEMETOREMENALIZKTILJER ROTO
 67: Mismatolins 67; things
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 SEQUENCE FROM N.A.
FINAMI Y. FUNABIKI K.. SATO K.;
FINAMI Y. FUNABIKI K.. SATO K.;
STRAL AND SASSAS I DIZZINENJ.
FINASILE. PSO0107; PROTEIN_KINASE_AIP; 1.
PROSITE: PSO0107; PROTEIN_KINASE_TYP; 1.
PROM: PROTEIN_KINASE_TYP; 1.
 01-001.1997 (TREMBLREL. 04, CREATED)
01-001.1997 (TREMBLREL. 04, IAST SECTEMBLE DIVATE)
31-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION HEDATE)
 PEAN: PEOUSE SH3.
PFAM: PEOUSE PAINASE.
SECUENCE 512 AA: 58412 MW: 12HOHA65 CPC42:
 42.6%, Scorp Rn4, 19, 10, 10, 14, 18, Pred, No. 5,530-155;
 PFAM: PF00069; pkinase.
SEOUENCE 488 AA: 55794 MW; HICDE550 CHC12;
 PRT: 488 AA
 PROSITE: PS00107; PROTEIN_KINASE_AII: PROSITE: PS00109: PPOTEIN_KINASE_IYR; }
 MEDLINE: 0418714,
WRIGHT D , SEFTON B.M., RAMPS M.P.,
WRIGHT D 1 42429-2437 (1994),
EMBL, U07236, G460966,
PROSITE: PS00107: PROTEIN_KINASE_AIF;
 LYN PROTEIN TYROSINE KINASE.
 est bocal Similarity 44.18;
atches 113; Conservative
 486 DRPIFDYLRSVLEDF 500
 PRELIMINARY;
 239 MRPSFLQLREQLEHI 253
 SEUUENCE FROM N.A.
 PFAM: PFOOOTT; SH2
 I SSUE-LEUKEMIA
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123 ROLAABONLUSEDINGANSDEGLIP - FASSETITIONSENTAPEALEERESSIKSEV 179
 119 WAS STILLMENVILSANTIE SMÄNEDVILMINENSEMMARKEICHEELNAVIAEUMRARFE 478
 SCT_ABACKWAYS WANG TO THE THE TANK THE WAY THE TANK THE THE TANK THE THE THE TANK TH
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 *)] AVVI--KERIYIVIEVMARGOLLDFIKTJEGSRISIPRILIBMSAQIAEGMAYIEFMNSIH 358
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 CON BUILDEOUNTED AMELINE DESERVATOR OF THE STREET AND THE
 5 INTIGITAROSTORYANDONEAN KVANNOTRADA-TAQAEDAEASVYTTERSKINGIL 60
 unery Match
Best Loval Similarity 43.98, Pref No. 4.55e-153,
Matthew 112, Consentation 69, Misharither 56, Tedels 8, Gaps
 12.2 BROLAABAULUSELINGAVARUSTELINGA - CASSATAINTAKLAVERATERA EERMERATERA
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Himo sapidus (hyman).
etymastia: metaolni ohomomin: vortembria: tetbaroln: Manmalia:
 FRI. 238 AA. (6173)
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 TART SECUENCE TECATE)
LAST ANNOTABLES GEDATES
 PPAM: PECCOSS: SHA
PPAM: PECCOSS: pkinnse
SEQUENCE: 505 Ah. 57756 AM. 8560EF45 CR32;
 -N.V.1996 (TAPVRIBED OF CONTRACT OF CONTRA
 228 AMARRINGIADOLEHI 253
 441 HERPIFOYLGSVIDDF 476
 474 ERFTFEFLQSVLEDF 493
 249 MRPSFLOLREOLEHI 253
 PRELIXIMATE
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FAR SANYIHPOLAAPNVLVGOGNIVKIALFELARITELERE REVERETETEN BALGELAANDEK 421
 60 POSTIKADILPATILLYMASOVAAAMSYLESKGFTHRTILAARNILVGENHLIKVADFILARS 119
 89 BSRSESVIGGLIZKPSIDVZEAMYVEGNWRVHNILARITHTT TITTET TO THE 14P
 119 A.SS.-TQDIS-KIEVKWIAPEALRERMISIKSINWSFOLLIWETYSFORNTWPRITLM: 2:4
 120 MANDYYKAHSGAKFPIKWISPEALAYNKFSSKSDVWAFGVLMWEIVKYGASPYPBHLIN, 175
 1 AVKILKEDQIDVEBFIKEADMAKQIKHFNLVELIGVCIHE-SFITTITETMFEGNELETE 59
 30 AVKCIKNDAIA-QAFLAEASVATÇLEHSNLVÇLISVIVEEKGSLIIVTEHMAKSSLVDIL 38
 Query Match
Best Local Similarity 47.9%; Pred. No. 7.86e-153;
Matches 105, Conservative 54, Mismatches 54, Indels 6: Japs
 364 IQLYAVOTVEEP-IXIITELMKHSSLLEYLQAIASK3FSLKMQILJUMAAQIAAJSAN
 1 NMKELKLLQTIGKGEFGDVMLGDYRGNK-VAVKCIKNDAT-AQAFLAEASVE:
 244 DRISLKFVRKLGSGQFGDVWEGLWNNITPVALKTLKSGTMDPKLFLAEA, 1874
 Whery March 41.9%; Soure 706, 18-5; Length 517.
Best Local Similarity 43.3%; Pred. No. 7.86e-153;
Matches 113; Conservative 62, Mismatches 77, Indels
SERUENCE FROM N.A.
STRAIN-UCI;
STRAIN-UCI;
SHEMITER LE., SARACCHI M.,
SUBMITER (MAY 1998) TO EMET, OF BEANFOOTH, TOTAL PANKS.
BYEL, AFOCSTIL, 33153893;
TYROGINE-PROTEIN KINASE.
 01-FEE-1997 (IMEMBLREL 02, CREAIED)
01-FEE-1997 (IMEMBLREL, 02, LASI SEQUENCE UPDATE)
01-JUN-1998 (IMEMBLREL, 06, LASI ANNOTATION UPDATE)
DSRC41.
 DEOSOPHILA MELANOGASTER (FRUIT FLY).
EUKARYSTA, METAZGA, ARTHEGPÖDA; INSECIA; DIPTERA.
 PIC TIPOTAPHEGEBOGEDAAYELMIDOWFWNFHPFFTFF PIC
 DOT VVPEVERGYENDAFDGGFFAVYEVMENGWELDAAGETSE D43
 298 AA; 34613 MW, ACEST, CF 28030;
 PPT;
 PPELIMINAPY;
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 SECTENCE FROM N.A. STRAIN=CANTON S;
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TO FIST KRIVWSFILLIMELYSFORVPYPPHILLKHOVPHYEKOYKMDAPDGIEPAVTEVKNG 232
 1.0 BITTLERBITANGGFTAVVQLAÇMFTTYAVMILKEGAMSELEFVERQIMMKLSHPKLVKF 451
 452 v.vv. SEKREPITIVTEVITNGCLENVILKSHGKG-CES-COLLEMCYDVCESMAFLESHOF 508
 62 : WIVEEKGRIVITETMAKSSLVPYLRSBGRSVLAGDG-LLKFSLDVGEAHHYLEGNNF 120
 ANY THROLAARNOLVDSDLSVKVSDEGMTRYVLDDQYVSSVGTKEPVKWSAPEVFHYFKYSSK 568
 . . VHR. LAARNVI VSETINVAKVSDEGLIKEASSTG--DI-G-KLPVKWIAPEALREKKESIK 176
 TO STAWAFGILMWEVESTORL PYDLYDNSEVVVKUSOGHRLYRPQLASDTIYQLMYSOWHEL 628
 STWESTSTIAMETYSPORVPYPRIPLEDVVFRVERGTENTAPEGGFFAVYEVERHED 236
 4 ELKOLOTIORGEFONWEGNYRGN FVANWOIRNDATAGA FLAEARWITCLSHENLYCL 61
 March 41.7%; Score 741; DB II; Lendth 651; coul Similarity 43.7%; Prod. No. 1.20e-151; s. 114; Conservative 63; Mismatches 74; Indels 10; Caps
 MTS MTSTILTS (METSE).
HTANN TAL MHTAZ AL DE HLATAL VERTERRATAL TETRAPODAL MAMMALTAL
HTTHEBIAL BETERNIA.
 SECTION BETWOON N.A. STEEPINE MARROW: STEALY STRUKEN A. CALTERRAL M., LI C.L.; STRUKEL D., POWER M.A., CALTERRAL M., LI C.L.; STRUKELTEN (FERFEREN) TO EMPLY CONFAMENDED DATA BANKS.
 |-WAY-|GAY (TREMHUBEL, G), CREATED|
|-WAY-|GAY (TREMHUBEL, G), LAST SEQUENCE UPDATE|
|-WAY-|GAY (TREMHUBEL, G), LAST SEQUENCE UPDATE)
|-WAY-|GAY (TREMHUBEL, G), LAST ANNOTATION (FDATE)
 SECTION 1 CANADA MATERIAL MATE
 PRT: 651 AA.
 Sourch completed: Word Jan 13 12:19:52 1999
 143 WHKOPMREPTFUTTOWKLEDF 503
 - * WHILDAAMRPSFILDINELIEHI 253
 624 PEKEPTECOLLISALEPLRECD 649
 2 CT AAMRPSPICLREQUEHIKTHE 257
 PRELLMINARY
 SECTENTE FROM N.A.
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